GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

Run on: May 21, 2003, 18:39:49 ; Search time 27 Seconds
(without alignments)
1150.584 Million cell updates/sec

Title: US-09-913-955A-1
Perfect score: 3958
Sequence: 1 MEAETGSSVETGKKANRGTR.....AFNCPPNSTMNRGMDSCRLW 749

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3952	99.8	749	1	PEX_HUMAN	P78562 homo sapien
2	3837	96.9	749	1	PEX_MOUSE	P70669 mus musculu
3	1283.5	32.4	749	1	NEP_HUMAN	P08473 homo sapien
4	1270.5	32.1	749	1	NEP_RABIT	P08049 oryctolagus
5	1263.5	31.9	749	1	NEP_RAT	P07861 rattus norv
6	1262.5	31.9	754	1	ECE1_CAVPO	P97739 cavia porce
7	1259.5	31.8	749	1	NEP_MOUSE	Q61391 mus musculu
8	1257	31.8	770	1	ECE1_HUMAN	P42892 homo sapien
9	1243.5	31.4	762	1	ECE1_RAT	P42893 rattus norv
10	1241.5	31.4	754	1	ECE1_BOVIN	P42891 bos taurus
11	1221	30.8	787	1	ECE2_HUMAN	O60344 homo sapien
12	1184	29.9	787	1	ECE2_BOVIN	Q10711 bos taurus
13	992	25.1	775	1	ECEL_MOUSE	Q9jmi0 mus musculu
14	977	24.7	775	1	ECEL_RAT	Q9jhl3 rattus norv
15	969.5	24.5	775	1	ECEL_HUMAN	O95672 homo sapien
16	949	24.0	769	1	YCYL_CAEEL	Q22523 caenorhabdi
17	597.5	15.1	732	1	KELL_HUMAN	P23276 homo sapien
18	586	14.8	647	1	PEPO_LACHE	O52071 lactobacill
19	495	12.5	626	1	PEPO_LACLA	Q07744 lactococcus
20	494	12.5	626	1	PEPO_LACLC	Q09145 lactococcus
21	365	9.2	564	1	YSC6_STRGC	P42359 streptococc
22	135.5	3.4	2077	1	TEGU_HSV6U	P52340 human herpe
23	135	3.4	853	1	NAT1_YEAST	P12945 saccharomyc
24	126.5	3.2	2077	1	TEGU_HSV6G	P30002 human herpe
25	126	3.2	1545	1	YMH2_YEAST	Q03640 saccharomyc
26	121	3.1	490	1	Y032_BORBU	O51063 borrelia bu
27	120	3.0	863	1	GYRA_CAMJE	Q03470 campylobact
28	117	3.0	408	1	YZ33_METJA	Q60290 methanococc
29	117	3.0	700	1	RIR1_BACSU	P50620 bacillus su
30	116.5	2.9	1270	1	VGLN_CHICK	P81021 gallus gall
31	116.5	2.9	1616	1	VIT1_CAEEL	P55155 caenorhabdi
32	116.5	2.9	1790	1	VIT_ANTGR	Q05808 anthonomus
33	116	2.9	725	1	RIR1_MYCTU	P50640 mycobacteri
34	116	2.9	3587	1	SRF1_BACSU	P27206 bacillus su
35	115	2.9	882	1	RA50_PYRFU	P58301 pyrococcus
36	114.5	2.9	3061	1	POLG_PVYHU	Q02963 p genome po
37	114	2.9	762	1	MNN1_YEAST	P39106 saccharomyc
38	114	2.9	2059	1	TEGU_HSV7J	P52362 human herpe
39	113.5	2.9	986	1	EPIB_STAEP	P30195 staphylococ
40	112.5	2.8	1826	1	SUIS_RABIT	P07768 oryctolagus
41	112	2.8	1295	1	BXA2_CLOBO	Q45894 clostridium
42	111.5	2.8	1056	1	SPS_SPIOL	P31928 spinacia ol
43	111.5	2.8	1230	1	SMC3_YEAST	P47037 saccharomyc
44	111	2.8	1328	1	EXO2_SCHPO	P40383 schizosacch
45	110	2.8	1638	1	BRM_DROME	P25439 drosophila

ALIGNMENTS

RESULT 1
PEX_HUMAN
ID PEX_HUMAN STANDARD; PRT; 749 AA.
AC P78562; O00678; Q99827; Q13646; Q93032;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Phosphate regulating neutral endopeptidase (EC 3.4.24.-)
DE (Metalloendopeptidase homolog PEX) (X-linked hypophosphatemia protein)
DE (HYP) (Vitamin D-resistant hypophosphatemic rickets protein).
GN PHEX OR PEX.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND VARIANTS HYP ARG-85; LEU-534; ARG-579 AND
RP PRO-651.
RX MEDLINE=97343325; PubMed=9199930;
RA Francis F., Strom T.M., Hennig S., Boeddrich A., Lorenz B.,
RA Brandau O., Mohnike K.L., Cagnoli M., Steffens C., Klages S.,
RA Borzym K., Pohl T., Oudet C.L., Econs M.J., Rowe P.S.N., Reinhardt R.,
RA Meitinger T., Lehrach H.;
RT "Genomic organization of the human PEX gene mutated in X-linked
RT dominant hypophosphatemic rickets.";
RL Genome Res. 7:573-585(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97232252; PubMed=9077527;
RA Beck L., Soumounou Y., Martel J., Krishnamurthy G., Gauthier C.,
RA Goodyer C.G., Tenenhouse H.S.;
RT "Pex/PEX tissue distribution and evidence for a deletion in the 3'
RT region of the Pex gene in X-linked hypophosphatemic mice.";
RL J. Clin. Invest. 99:1200-1209(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone;
RX MEDLINE=97343443; PubMed=9199999;
RA Guo R., Quarles L.D.;
RT "Cloning and sequencing of human PEX from a bone cDNA library:
RT evidence for its developmental stage-specific regulation in
RT osteoblasts.";
RL J. Bone Miner. Res. 12:1009-1017(1997).
RN [4]
RP SEQUENCE FROM N.A.
RA Lipman M.L., Panda D., Henderson J.E., Shen Y., Goltzman D.,
RA Karaplis A.C.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=97224400; PubMed=9070861;
RA Grieff M., Mumm S., Waeltz P., Mazzarella R., Whyte M.P.,
RA Thakker R.V., Schlessinger D.;
RT "Expression and cloning of the human X-linked hypophosphatemia gene
RT cDNA.";
RL Biochem. Biophys. Res. Commun. 231:635-639(1997).

RN [6]
RP SEQUENCE OF 4-641 FROM N.A.
RX MEDLINE=96024647; PubMed=7550339;
RA Francis F., Hennig S., Korn B., Reinhardt R., de Jong P., Poustka A.,
RA Lehrach H., Rowe P.S.N., Goulding J.N., Summerfield T., Mountford R.,
RA Read A.P., Popowska E., Pronicka E., Davies K.E., Oriordan J.L.H.,
RA Econs M.J., Nesbitt T., Drezner M.K., Oudet C.L., Pannetier S.,
RA Hanauer A., Strom T.M., Meindl A., Lorenz B., Cagnoli M.,
RA Mohnike K.L., Murken J., Meitinger T.;
RT "A gene (PEX) with homologies to endopeptidases is mutated in
RT patients with X-linked hypophosphatemic rickets. The HYP
RT Consortium.";
RL Nat. Genet. 11:130-136(1995).
RN [7]
RP SEQUENCE OF 1-116 FROM N.A.
RA Waterston R.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
RN [8]
RP VARIANTS HYP TYR-85; CYS-166; SER-252; ILE-253 AND VAL-579.
RX MEDLINE=97260404; PubMed=9106524;
RA Holm I.A., Huang X., Kunkel L.M.;
RT "Mutational analysis of the PEX gene in patients with X-linked
RT hypophosphatemic rickets.";
RL Am. J. Hum. Genet. 60:790-797(1997).
RN [9]
RP VARIANTS HYP SER-77; PRO-138; LEU-534 AND ARG-579.
RX MEDLINE=97252387; PubMed=9097956;
RA Rowe P.S.N., Oudet C.L., Francis F., Sinding C., Pannetier S.,
RA Econs M.J., Strom T.M., Meitinger T., Garabedian M., David A.,
RA Macher M.-A., Questiaux E., Popowska E., Pronicka E., Read A.P.,
RA Mokrzycki A., Glorieux F.H., Drezner M.K., Hanauer A., Lehrach H.,
RA Goulding J.N., O'Riordan J.L.H.;
RT "Distribution of mutations in the PEX gene in families with X-linked
RT hypophosphataemic rickets (HYP).";
RL Hum. Mol. Genet. 6:539-549(1997).
RN [10]
RP VARIANT HYP PRO-555.
RX MEDLINE=98439582; PubMed=9768646;
RA Econs M.J., Friedman N.E., Rowe P.S.N., Speer M.C., Francis F.,
RA Strom T.M., Oudet C.L., Smith J.A., Ninomiya J.T., Lee B.E.,
RA Bergen H.;
RT "A PHEX gene mutation is responsible for adult-onset vitamin
RT D-resistant hypophosphatemic osteomalacia: evidence that the disorder
RT is not a distinct entity from X-linked hypophosphatemic rickets.";
RL J. Clin. Endocrinol. Metab. 83:3459-3462(1998).
RN [11]
RP VARIANTS HYP F-317; L-534; R-579; R-621; N-680 DEL; T-720; Y-731 AND
RP R-749.
RX MEDLINE=98439610; PubMed=9768674;
RA Dixon P.H., Christie P.T., Wooding C., Trump D., Grieff M., Holm I.A.,
RA Gertner J.M., Schmidtke J., Shah B., Shaw N., Smith C., Tau C.,
RA Schlessinger D., Whyte M.P., Thakker R.V.;
RT "Mutational analysis of PHEX gene in X-linked hypophosphatemia.";
RL J. Clin. Endocrinol. Metab. 83:3615-3623(1998).
RN [12]
RP VARIANTS HYP S-80; F-142; G-237; C-530; D-573; S-733 AND W-746.
RX MEDLINE=99368844; PubMed=10439971;
RA Filisetti D., Ostermann G., von Bredow M., Strom T.M., Filler G.,
RA Ehrich J., Pannetier S., Garnier J.-M., Rowe P.S.N., Francis F.,
RA Julienne A., Hanauer A., Econs M.J., Oudet C.L.;
RT "Non-random distribution of mutations in the PHEX gene, and
RT under-detected missense mutations at non-conserved residues.";
RL Eur. J. Hum. Genet. 7:615-619(1999).
RN [13]
RP VARIANTS HYP F-85; P-141; V-341 DEL; P-567; K-680 AND Y-693.
RX MEDLINE=20202840; PubMed=10737991;
RA Tyynismaa H., Kaitila I., Naentoe-Salonen K., Ala-Houhala M.,
RA Alitalo T.;
RT "Identification of fifteen novel PHEX gene mutations in Finnish
RT patients with hypophosphatemic rickets.";
RL Hum. Mutat. 15:383-384(2000).
RN [14]
RP VARIANTS HYP ARG-160 AND ASN-444 INS.
RX MEDLINE=20461419; PubMed=11004247;
RA Sato K., Tajima T., Nakae J., Adachi M., Asakura Y., Tachibana K.,
RA Suwa S., Katsumata N., Tanaka T., Hayashi Y., Abe S., Murashita M.,
RA Okuhara K., Shinohara N., Fujieda K.;
RT "Three novel PHEX gene mutations in Japanese patients with X-linked
RT hypophosphatemic rickets.";
RL Pediatr. Res. 48:536-540(2000).
CC -!- FUNCTION: PROBABLY INVOLVED IN BONE AND DENTIN MINERALIZATION
CC AND RENAL PHOSPHATE REABSORPTION.
CC -!- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
CC -!- TISSUE SPECIFICITY: LYMPHOCYTE AND FETAL BRAIN; NOT IN ADULT
CC BRAIN, PLACENTA, SKELETAL MUSCLE, AND PANCREAS; NOT IN ADULT AND
CC FETAL HEART, LUNG, LIVER, AND KIDNEY.
CC -!- DISEASE: DEFECTS IN PHEX ARE A CAUSE OF X-LINKED HYPOPHOSPHATEMIC
CC RICKETS (HYP), A DOMINANT DISORDER CHARACTERIZED BY IMPAIRED
CC PHOSPHATE UPTAKE IN THE KIDNEY, WHICH IS LIKELY TO BE CAUSED BY
CC ABNORMAL REGULATION OF SODIUM PHOSPHATE COTRANSPORT IN THE
CC PROXIMAL TUBULES. CLINICAL MANIFESTATIONS INCLUDE SKELETAL
CC DEFORMITIES, GROWTH FAILURE, CRANIOSYNOSTOSIS, PARAVERTEBRAL
CC CALCIFICATIONS, PSEUDOFRACTURES IN LOWER EXTREMITIES, AND MUSCULAR
CC HYPOTONIA WITH ONSET IN EARLY CHILDHOOD. X-LINKED HYPOPHOSPHATEMIC
CC RICKETS IS THE MOST COMMON FORM OF HYPOPHOSPHATEMIA WITH AN
CC INCIDENCE OF 1 IN 20000.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M13.
CC -!- DATABASE: NAME=PHEXdb; WWW="http://data.mch.mcgill.ca/phexdb/".
CC --

CC --
DR EMBL; Y10196; CAA71258.1; -.
DR EMBL; U75645; AAB47749.1; -.
DR EMBL; U82970; AAC24487.1; -.
DR EMBL; U87284; AAB47562.1; -.
DR EMBL; Y08111; CAA69326.1; -.
DR EMBL; Y08112; CAA69326.1; JOINED.
DR EMBL; Y08113; CAA69326.1; JOINED.
DR EMBL; Y08114; CAA69326.1; JOINED.
DR EMBL; Y08115; CAA69326.1; JOINED.
DR EMBL; Y08116; CAA69326.1; JOINED.
DR EMBL; Y08117; CAA69326.1; JOINED.
DR EMBL; Y08118; CAA69326.1; JOINED.
DR EMBL; Y08119; CAA69326.1; JOINED.
DR EMBL; Y08120; CAA69326.1; JOINED.
DR EMBL; Y08121; CAA69326.1; JOINED.
DR EMBL; Y08122; CAA69326.1; JOINED.
DR EMBL; Y08123; CAA69326.1; JOINED.
DR EMBL; Y08124; CAA69326.1; JOINED.
DR EMBL; Y08125; CAA69326.1; JOINED.
DR EMBL; Y08126; CAA69326.1; JOINED.
DR EMBL; Y08127; CAA69326.1; JOINED.
DR EMBL; Y08128; CAA69326.1; JOINED.
DR EMBL; Y08129; CAA69326.1; JOINED.
DR EMBL; Y08130; CAA69326.1; JOINED.
DR EMBL; Y08131; CAA69326.1; JOINED.
DR EMBL; Y08132; CAA69326.1; JOINED.
DR EMBL; U81183; AAB42219.1; -.
DR EMBL; U81167; AAB42219.1; JOINED.
DR EMBL; U81168; AAB42219.1; JOINED.
DR EMBL; U81169; AAB42219.1; JOINED.
DR EMBL; U81171; AAB42219.1; JOINED.
DR EMBL; U81172; AAB42219.1; JOINED.
DR EMBL; U81173; AAB42219.1; JOINED.
DR EMBL; U81174; AAB42219.1; JOINED.
DR EMBL; U81175; AAB42219.1; JOINED.
DR EMBL; U81176; AAB42219.1; JOINED.
DR EMBL; U81177; AAB42219.1; JOINED.
DR EMBL; U81178; AAB42219.1; JOINED.
DR EMBL; U81179; AAB42219.1; JOINED.

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 Query Match             99.8%;  Score 3952;  DB 1;  Length 749;
 Best Local Similarity   99.9%;  Pred. No. 2.7e-258;
 Matches  748;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 MEAETGSSVETGKKANRGTRIALVVFVGGTLVLGTILFLVSQGLLSLQAKQEYCLKPECI 60
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Db       1 MEAETGSSVETGKKANRGTRIALVVFVGGTLVLGTILFLVSQGLLSLQAKQEYCLKPECI 60

Qy      61 EAAAAILSKVNLSVDPCDNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLE 120
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Db      61 EAAAAILSKVNLSVDPCDNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLE 120

Qy     121 KSISRRRDTEAIQKAKILYSSCMNEKAIEKADAKPLLHILRHSPFRWPVLESNIGPEGVW 180
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Db     121 KSISRRRDTEAIQKAKILYSSCMNEKAIEKADAKPLLHILRHSPFRWPVLESNIGPEGVW 180

Qy     181 SERKFSLLQTLATFRGQYSNSVFIRLYVSPDDKASNEHILKLDQATLSLAVREDYLDNST 240
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Db     181 SERKFSLLQTLATFRGQYSNSVFIRLYVSPDDKASNEHILKLDQATLSLAVREDYLDNST 240

Qy     241 EAKSYRDALYKFMVDTAVLLGANSSRAEHDMKSVLRLEIKIAEIMIPHENRTSEAMYNKM 300
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Db     241 EAKSYRDALYKFMVDTAVLLGANSSRAEHDMKSVLRLEIKIAEIMIPHENRTSEAMYNKM 300

Qy     301 NISELSAMIPQFDWLGYIKKVIDTRLYPHLKDISPSENVVVRVPQYFKDLFRILGSERKK 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 NISELSAMIPQFDWLGYIKKVIDTRLYPHLKDISPSENVVVRVPQYFKDLFRILGSERKK 360

Qy     361 TIANYLVWRMVYSRIPNLSRRFQYRWLEFSRVIQGTTTLLPQWDKCVNFIESALPYVVGK 420
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Db     361 TIANYLVWRMVYSRIPNLSRRFQYRWLEFSRVIQGTTTLLPQWDKCVNFIESALPYVVGK 420

Qy     421 MFVDVYFQEDKKEMMEELVEGVRWAFIDMLEKENEWMDAGTKRKAKEKARAVLAKVGYPE 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 MFVDVYFQEDKKEMMEELVEGVRWAFIDMLEKENEWMDAGTKRKAKEKARAVLAKVGYPE 480

Qy     481 FIMNDTHVNEDLKAIKFSEADYFGNVLQTRKYLAQSDFFWLRKAVPKTEWFTNPTTVNAF 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 FIMNDTHVNEDLKAIKFSEADYFGNVLQTRKYLAQSDFFWLRKAVPKTEWFTNPTTVNAF 540

Qy     541 YSASTNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNGRKYDKNGNLD 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 YSASTNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNGRKYDKNGNLD 600

Qy     601 PWWSTESEEKFKEKTKCMINQYSNYYWKKAGLNVKGKRTLGENIADNGGLREAFRAYRKW 660
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Db     601 PWWSTESEEKFKEKTKCMINQYSNYYWKKAGLNVKGKRTLGENIADNGGLREAFRAYRKW 660

Qy     661 INDRRQGLEEPLLPGITFTNNQLFFLSYAHVRCNSYRPEAAREQVQIGAHSPPQFRVNGA 720
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Db     661 INDRRQGLEEPLLPGITFTNNQLFFLSYAHVRCNSYRPEAAREQVQIGAHSPPQFRVNGA 720

Qy     721 ISNSEEFQKAFNCPPNSTMNRGMDSCRLW 749
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Db     721 ISNFEEFQKAFNCPPNSTMNRGMDSCRLW 749
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RESULT 2
PEX_MOUSE
ID   PEX_MOUSE       STANDARD;       PRT;   749 AA.
AC   P70669; P97439;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Metalloendopeptidase homolog PEX (EC 3.4.24.-) (Phosphate regulating
DE   neutral endopeptidase) (X-linked hypophosphatemia protein) (HYP)
DE   (Vitamin D-resistant hypophosphatemic rickets protein).
GN   PHEX OR PEX OR HYP.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96411643; PubMed=8812412;
RA   Du L., Desbarats M., Viel J., Glorieux F.H., Cawthorn C., Ecarot B.;
RT   "cDNA cloning of the murine Pex gene implicated in X-linked
RT   hypophosphatemia and evidence for expression in bone.";
RL   Genomics 36:22-28(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97217775; PubMed=9063736;
RA   Strom T.M., Francis F., Lorenz B., Boeddrich A., Econs M.J.,
RA   Lehrach H., Meitinger T.;
RT   "Pex gene deletions in Gy and Hyp mice provide mouse models for
RT   X-linked hypophosphatemia.";
RL   Hum. Mol. Genet. 6:165-171(1997).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J;
RX   MEDLINE=97232252; PubMed=9077527;
RA   Beck L., Soumounou Y., Martel J., Krishnamurthy G., Gauthier C.,
RA   Goodyer C.G., Tenenhouse H.S.;
RT   "Pex/PEX tissue distribution and evidence for a deletion in the 3'
RT   region of the Pex gene in X-linked hypophosphatemic mice.";
RL   J. Clin. Invest. 99:1200-1209(1997).
CC   -!- FUNCTION: PROBABLY INVOLVED IN BONE AND DENTIN MINERALIZATION
CC       AND RENAL PHOSPHATE REABSORPTION.
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
CC   -!- TISSUE SPECIFICITY: BONE.
CC   -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M13.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U49908; AAC36502.1; -.
DR   EMBL; U73910; AAC25962.1; -.
DR   EMBL; U73912; AAC25964.1; -.
DR   EMBL; U73913; AAC25965.1; -.
DR   EMBL; U73914; AAC25966.1; -.
DR   EMBL; U73911; AAC25963.1; -.
DR   EMBL; U73915; AAC25967.1; -.
DR   EMBL; U75646; AAB47750.1; -.
DR   HSSP; P08473; 1DMT.
DR   MEROPS; M13.091; -.
DR   MGD; MGI:107489; Phex.
DR   InterPro; IPR000718; Peptidase_M13.
DR   InterPro; IPR001230; Prenyl_site.
DR   InterPro; IPR000130; Zn_MTpeptdse.
DR   Pfam; PF01431; Peptidase_M13; 1.
DR   PRINTS; PR00786; NEPRILYSIN.
DR   PROSITE; PS00142; ZINC_PROTEASE; 1.
KW   Hydrolase; Metalloprotease; Zinc; Glycoprotein; Transmembrane;
KW   Signal-anchor.
FT   DOMAIN        1     20       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     21     37       SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT                                (POTENTIAL).
FT   DOMAIN       38    749       EXTRACELLULAR (POTENTIAL).
FT   METAL       580    580       ZINC (CATALYTIC) (BY SIMILARITY).
FT   ACT_SITE    581    581       BY SIMILARITY.
FT   METAL       584    584       ZINC (CATALYTIC) (BY SIMILARITY).
FT   METAL       642    642       ZINC (CATALYTIC) (BY SIMILARITY).
FT   ACT_SITE    646    646       PROTON DONOR (POTENTIAL).
FT   CARBOHYD     71     71       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    238    238       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    263    263       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    290    290       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    301    301       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    377    377       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    484    484       N-LINKED (GLCNAC. . .) (POTENTIAL).
```

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FT   CARBOHYD    736    736       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT    430    430       D -> V (IN REF. 3).
SQ   SEQUENCE   749 AA;  86418 MW;  A88FA481C376C18A CRC64;

  Query Match             96.9%;  Score 3837;  DB 1;  Length 749;
  Best Local Similarity   95.9%;  Pred. No. 1.5e-250;
  Matches  718;  Conservative   20;  Mismatches   11;  Indels    0;  Gaps    0;

Qy       1 MEAETGSSVETGKKANRGTRIALVVFVGGTLVLGTILFLVSQGLLSLQAKQEYCLKPECI 60
           |||||||::||||  ||| |||| :|:|||||||||:|||||||||| ||||||||||||
Db       1 MEAETGSTMETGKGTNRGIRIALALFIGGTLVLGTLLFLVSQGLLSFQAKQEYCLKPECI 60

Qy      61 EAAAAILSKVNLSVDPCDNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLE 120
           ||||||:||||||||||:|||||||||||||||||||||||||||||||||||||||||| |||
Db      61 EAAAAIMSKVNLSVDPCENFFRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKALLE 120

Qy     121 KSISRRRDTEAIQKAKILYSSCMNEKAIEKADAKPLLHILRHSPFRWPVLESNIGPEGVW 180
           ||:|||||||:|||||||||||||||||||||||||||||||||||||||||:|||||||
Db     121 KSVSRRRDTEAVQKAKILYSSCMNEKAIEKADAKPLLHILRHSPFRWPVLEANIGPEGVW 180

Qy     181 SERKFSLLQTLATFRGQYSNSVFIRLYVSPDDKASNEHILKLDQATLSLAVREDYLDNST 240
           |||||||||||||||||||||||||||||||||||||||||||||||||||:|||:|
Db     181 SERKFSLLQTLATFRGQYSNSVFIRLYVSPDDKASNEHILKLDQATLSLAVREDFLDNTT 240

Qy     241 EAKSYRDALYKFMVDTAVLLGANSSRAEHDMKSVLRLEIKIAEIMIPHENRTSEAMYNKM 300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 EAKSYRDALYKFMVDTAVLLGANSSRAEHDMKSVLRLEIKIAEIMIPHENRTSEAMYNKM 300

Qy     301 NISELSAMIPQFDWLGYIKKVIDTRLYPHLKDISPSENVVVRVPQYFKDLFRILGSERKK 360
           |||||||||||||||||||||||||||||| ||||||||||||||||||:||||
Db     301 NISELSAMIPQFDWLGYIKKVIDTRLYPHLKDIGPSENVVVRVPQYFKDLFRILGAERKK 360

Qy     361 TIANYLVWRMVYSRIPNLSRRFQYRWLEFSRVIQGTTTLLPQWDKCVNFIESALPYVVGK 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 TIANYLVWRMVYSRIPNLSRRFQYRWLEFSRVIQGTTTLLPQWDKCVNFIESALPYVVGK 420

Qy     421 MFVDVYFQEDKKEMMEELVEGVRWAFIDMLEKENEWMDAGTKRKAKEKARAVLAKVGYPE 480
           |||:|:|||||||||||:|||||||||||||||||||||||||||:|||||||||||||||
Db     421 MFVNVHFQEDKKEMMEELIEGVRWAFIDMLEKENEWMDAGTKRKAQEKARAVLAKVGYPE 480

Qy     481 FIMNDTHVNEDLKAIKFSEADYFGNVLQTRKYLAQSDFFWLRKAVPKTEWFTNPTTVNAF 540
           ||||||:|||||||||||:|||||||||||||||||||||||||||||||||||||||||||
Db     481 FIMNDTYVNEDLKAIKFSESDYFGNVLQTRKYLAQSDFFWLRKAVPKTEWFTNPTTVNAF 540

Qy     541 YSASTNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNGRKYDKNGNLD 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 YSASTNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNGRKYDKNGNLD 600

Qy     601 PWWSTESEEKFKEKTKCMINQYSNYYWKKAGLNVKGKRTLGENIADNGGLREAFRAYRKW 660
           |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 PWWSVESEEKFKEKTKCMINQYSNYYWKKAGLNVKGKRTLGENIADNGGLREAFRAYRKW 660

Qy     661 INDRRQGLEEPLLPGITFTNNQLFFLSYAHVRCNSYRPEAAREQVQIGAHSPPQFRVNGA 720
           |||||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 INDRRQGVEEPLLPGITFTNNQLFFLSYAHVRCNSYRPEAAREQVQIGAHSPPQFRVNGA 720

Qy     721 ISNSEEFQKAFNCPPNSTMNRGMDSCRLW 749
           ||| |||||||||| ||||||| ||||||
Db     721 ISNFEEFQKAFNCPRNSTMNRGADSCRLW 749


RESULT 3
NEP_HUMAN
ID   NEP_HUMAN       STANDARD;       PRT;   749 AA.
AC   P08473;
DT   01-AUG-1988 (Rel. 08, Created)
DT   01-AUG-1988 (Rel. 08, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Neprilysin (EC 3.4.24.11) (Neutral endopeptidase) (NEP)
DE   (Enkephalinase) (Common acute lymphocytic leukemia antigen) (CALLA)
DE   (Neutral endopeptidase 24.11) (CD10).
GN   MME OR EPN.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE OF 2-749 FROM N.A.
RC   TISSUE=Placenta;
RX   MEDLINE=88152222; PubMed=3162217;
RA   Malfroy B., Kuang W.-J., Seeburg P.H., Mason A.J., Schofield P.R.;
RT   "Molecular cloning and amino acid sequence of human enkephalinase
RT   (neutral endopeptidase).";
RL   FEBS Lett. 229:206-210(1988).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RX   MEDLINE=89010526; PubMed=2971756;
RA   Letarte M., Vera S., Tran R., Addis J.B.L., Onizuka R.J.,
RA   Quackenbush E.J., Jongeneel C.V., McInnes R.R.;
RT   "Common acute lymphocytic leukemia antigen is identical to neutral
RT   endopeptidase.";
RL   J. Exp. Med. 168:1247-1253(1988).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88263038; PubMed=2968607;
RA   Shipp M.A., Richardson N.E., Sayre P.H., Brown N.R., Masteller E.L.,
RA   Clayton L.K., Ritz J., Reinherz E.L.;
RT   "Molecular cloning of the common acute lymphoblastic leukemia antigen
RT   (CALLA) identifies a type II integral membrane protein.";
RL   Proc. Natl. Acad. Sci. U.S.A. 85:4819-4823(1988).
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89386688; PubMed=2528730;
RA   D'Adamio L., Shipp M.A., Masteller E.L., Reinherz E.L.;
RT   "Organization of the gene encoding common acute lymphoblastic
RT   leukemia antigen (neutral endopeptidase 24.11): multiple miniexons
RT   and separate 5' untranslated regions.";
RL   Proc. Natl. Acad. Sci. U.S.A. 86:7103-7107(1989).
RN   [5]
RP   ACTIVE SITE ASP-650.
RX   MEDLINE=94222095; PubMed=8168535;
RA   Le Moual H., Dion N., Roques B.P., Crine P., Boileau G.;
RT   "Asp650 is crucial for catalytic activity of neutral endopeptidase
RT   24-11.";
RL   Eur. J. Biochem. 221:475-480(1994).
RN   [6]
RP   X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
RX   MEDLINE=20135972; PubMed=10669592;
RA   Oefner C., D'Arcy A., Hennig M., Winkler F.K., Dale G.E.;
RT   "Structure of human neutral endopeptidase (Neprilysin) complexed with
RT   phosphoramidon.";
RL   J. Mol. Biol. 296:341-349(2000).
CC   -!- FUNCTION: THERMOLYSIN-LIKE SPECIFICITY, BUT IS ALMOST CONFINED ON
CC       ACTING ON POLYPEPTIDES OF UP TO 30 AMINO ACIDS. BIOLOGICALLY
CC       IMPORTANT IN THE DESTRUCTION OF OPIOID PEPTIDES SUCH AS MET-
CC       AND LEU-ENKEPHALINS BY CLEAVAGE OF A GLY-PHE BOND.
CC   -!- CATALYTIC ACTIVITY: Preferential cleavage at the amino group of
CC       hydrophobic residues in insulin, casein, hemoglobin, and a number
CC       of other proteins and polypeptides.
CC   -!- COFACTOR: BINDS 1 ZINC ION.
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein.
CC   -!- DISEASE: IMPORTANT CELL SURFACE MARKER IN THE DIAGNOSTIC OF HUMAN
CC       ACUTE LYMPHOCYTIC LEUKEMIA.
CC   -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M13.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X07166; CAA30157.1; ALT_INIT.
DR   EMBL; Y00811; CAA68752.1; -.
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DR   EMBL; J03779; AAA51915.1; -.
DR   EMBL; M26628; AAA52294.1; -.
DR   EMBL; M26607; AAA52294.1; JOINED.
DR   EMBL; M26608; AAA52294.1; JOINED.
DR   EMBL; M26609; AAA52294.1; JOINED.
DR   EMBL; M26610; AAA52294.1; JOINED.
DR   EMBL; M26611; AAA52294.1; JOINED.
DR   EMBL; M26612; AAA52294.1; JOINED.
DR   EMBL; M26613; AAA52294.1; JOINED.
DR   EMBL; M26614; AAA52294.1; JOINED.
DR   EMBL; M26615; AAA52294.1; JOINED.
DR   EMBL; M26616; AAA52294.1; JOINED.
DR   EMBL; M26617; AAA52294.1; JOINED.
DR   EMBL; M26618; AAA52294.1; JOINED.
DR   EMBL; M26619; AAA52294.1; JOINED.
DR   EMBL; M26620; AAA52294.1; JOINED.
DR   EMBL; M26621; AAA52294.1; JOINED.
DR   EMBL; M26622; AAA52294.1; JOINED.
DR   EMBL; M26623; AAA52294.1; JOINED.
DR   EMBL; M26624; AAA52294.1; JOINED.
DR   EMBL; M26625; AAA52294.1; JOINED.
DR   EMBL; M26626; AAA52294.1; JOINED.
DR   EMBL; M26627; AAA52294.1; JOINED.
DR   PIR; A41387; HYHUN.
DR   PDB; 1DMT; 20-DEC-00.
DR   MEROPS; M13.001; -.
DR   Genew; HGNC:7154; MME.
DR   MIM; 120520; -.
DR   InterPro; IPR000718; Peptidase_M13.
DR   InterPro; IPR001230; Prenyl_site.
DR   InterPro; IPR000130; Zn_MTpeptdse.
DR   Pfam; PF01431; Peptidase_M13; 1.
DR   PRINTS; PR00786; NEPRILYSIN.
DR   PROSITE; PS00142; ZINC_PROTEASE; 1.
KW   Hydrolase; Metalloprotease; Zinc; Transmembrane; Glycoprotein;
KW   Signal-anchor; 3D-structure.
FT   INIT_MET      0      0        CYTOPLASMIC (POTENTIAL).
FT   DOMAIN        1     27        SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT   TRANSMEM     28     50        (POTENTIAL).
FT                                 EXTRACELLULAR (POTENTIAL).
FT   DOMAIN       51    749        STOP-TRANSFER SEQUENCE (POTENTIAL).
FT   DOMAIN       15     22        FREE CARBOXYLATE OF SUBSTRATE
FT   BINDING     102    102        (BY SIMILARITY).
FT                                 ZINC (CATALYTIC).
FT   METAL       583    583        ZINC (CATALYTIC).
FT   METAL       587    587
FT   ACT_SITE    590    590        ZINC (CATALYTIC).
FT   METAL       646    646        PROTON DONOR.
FT   ACT_SITE    650    650        N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    144    144        N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    284    284        N-LINKED (GLCNAC. . .) (BY SIMILARITY).
FT   CARBOHYD    310    310        N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    324    324        N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    334    334        N-LINKED (GLCNAC. . .) (BY SIMILARITY).
FT   CARBOHYD    627    627        P -> R (IN REF. 3).
FT   CONFLICT     25     25        T -> R (IN REF. 3).
FT   CONFLICT     43     43        T -> R (IN REF. 3).
FT   CONFLICT     80     80        T -> R (IN REF. 3).
FT   CONFLICT    303    303
SQ   SEQUENCE   749 AA;  85382 MW;  55DE293A5439B0CB CRC64;

  Query Match          32.4%;  Score 1283.5;  DB 1;  Length 749;
  Best Local Similarity   35.9%;  Pred. No. 9.2e-79;
  Matches  272;  Conservative  155;  Mismatches  285;  Indels   45;  Gaps   19;

Qy      13 KKANRGTRIALVVFVGGTLVLGTILFLVSQGLLSLQAKQE--YCLKPECIEAAAAILSKV 70
           ||  | | : : : |   |||  :| :::  :::| |  :  |  :||::|| ::  :
Db      18 KKKQRWTPLEISLSV---LVL--LLTIIAVTMIALYATYDDGICKSSDCIKSAARLIQNM 72

Qy      71 NLSVDPCDNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLEKSISRRRDTE 130
           : : :|| :||::|| ||:  | |||    || :  ||  ::: ||::|::    :  |
Db      73 DATTEPCTDFFKYACGGWLKRNVIPETSSRYGNFDILRDELEVVLKDVLQE--PKTEDIV 130

Qy     131 AIQKAKILYSSCMNEKAIEKADAKPLLHILRHSPFRWPVLESNIGPEGVWSER---KFSL 187
           |:|||| || ||:|| ||:    :||| :|    : |||   |      | ::    ::
Db     131 AVQKAKALYRSCINESAIDSRGGEPLLKLL-PDIYGWPVATEN------WEQKYGASWTA 183

Qy     188 LQTLATFRGQYSNSVFIRLYVSPDDKASNEHILKLDQATLSLAVREDYLDNSTEAKSYRD 247
           : :|    :|   | | |:|  ||| |  |:: :||  | |  | || : :   |
Db     184 EKAIAQLNSKYGKKVLINLFVGTDDKNSVNHVIHIDQPRLGLPSR-DYYECTGIYKEACT 242

Qy     248 ALYKFMVDTAVL------LGANSSRAEHDMKSVLRLEIKIAEIMIPHENRTSE-AMYNKM 300
           |   ||:  | |       |  : ::   :|  |: || :||      |:|     :||||
Db     243 AYVDFMISVARLIRQEERLPIDENQLALEMNKVMELEKEIANATAKPEDRNDPMLLYNKM 302

Qy     301 NISELSAMI------PQFDWLGYIKKVIDTRLYPHLKDISPSENVVVRVPQYFKDLFRIL 354
           ::::              | || :  ::: |       |:  |:|||  |:|   |  ||
Db     303 TLAQIQNNFSLEINGKPFSWLNFTNEIMSTVNI----SITNEEDVVVYAPEYLTKLKPIL 358

Qy     355 GSERKKTIANYLVWRMVYSRIPNLSRRFQYRWLEFSRVIQGTTTLLPQWDKCVNFIESAL 414
           : : | : || :   : :||| ::     | : : |||:     | :| |::   :
Db     359 TKYSARDLQNLMSWRFIMDLVSSLSRTYKESRNAFRKALYGTTSETATWRRCANYVNGNM 418

Qy     415 PYVVGKMFVDVYFQEDKKEMMEELVEGVRWAFIDMLEKENEWMDAGTKRKAKEKARAVLA 474
           ||:::|:  |  : | ::|:|:  :|  ||  |: :  |||| ||::|:|||  |:
Db     419 ENAVGRLYVEAAFAGESKHVVEDLIAQIREVFIQTLD-DLTWMDAETKKRAEEKALAIKE 477

Qy     475 KVGYP-EFIMNDTHVNEDLKAIKFSEADYFGNVLQTRKYLAQSDFFWLRKAVPKTEWFTN 533
           ::||| : : ||  :| :   : : | :|| |::|  |:        ||: | | || :
Db     478 RIGYPDDIVSNDNKLNNEYLELNYKEDEYFENIIQNLKFSQSKQLKKLREKVDKDEWISG 537

Qy     534 PTTVNAFYSASTNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNGRKY 593
           ||||||:  ||| |||| || |||   :   ||:|| ||:::||| |||||:||| :
Db     538 AAVVNAFYSSGRNQIVFPAGILQPPFF-SAQQSNSLNYGGIGMVIGHEITHGFDDNGRNF 596

Qy     594 DKNGNLDPWWSTESEEKFKEKTKCMINQYSNYYWKKA-GLNVKGKRTLGENIADNGGLRE 652
           :|:|:|  ||: :|   |||:::||: || |: |  | | :: |  ||||||||||| :
Db     597 NKDGDLVDWWTQQSASNFKEQSQCMVYQYGNFSWDLAGGQHLNGINTLGENIADNGGLGQ 656

Qy     653 AFRAYRKWINDRRQGLEEPLLPGITFTNNQLFFLSYAHVRCNSYRPEAARE-QVQIGAHSP 712
           |:|||: :|  :: | || ||||:   : |||||::| | | :|||| |   ::   |||
Db     657 AYRAYQNYI--KKNG-EEKLLPGLDLNHKQLFFLNFAQVWCGTYRPEYAVNSIKTDVHSP 713

Qy     713 PQFRVNGAISNSEEFQKAFNCPPNSTMNRGMDSCRLW 749
           ||: | : || || :||:|  || ||     ||:|
Db     714 GNFRIIGTLQNSAEFSEAFHCRKNSYMN-PEKKCRVW 749


RESULT 4
NEP_RABIT
ID   NEP_RABIT      STANDARD;      PRT;   749 AA.
AC   P08049;
DT   01-AUG-1988 (Rel. 08, Created)
DT   01-AUG-1988 (Rel. 08, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Neprilysin (EC 3.4.24.11) (Neutral endopeptidase) (NEP)
DE   (Enkephalinase) (Neutral endopeptidase 24.11).
GN   MME.
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC   TISSUE=Kidney;
RX   MEDLINE=87275825; PubMed=2440677;
RA   Devault A., Lazure C., Nault C., le Moual H., Seidah N.G.,
RA   Chretien M., Kahn P., Powell J., Mallet J., Beaumont A., Roques B.P.,
RA   Crine P., Boileau G.;
RT   "Amino acid sequence of rabbit kidney neutral endopeptidase 24.11
RT   (enkephalinase) deduced from a complementary DNA.";
RL   EMBO J. 6:1317-1322(1987).
RN   [2]
RP   ERRATUM.
RA   Devault A., Lazure C., Nault C., le Moual H., Seidah N.G.,
RA   Chretien M., Kahn P., Powell J., Mallet J., Beaumont A., Roques B.P.,
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RA   Crine P., Boileau G.;
RL   EMBO J. 6:2506-2506(1987).
RN   [3]
RP   SEQUENCE OF 205-273 FROM N.A.
RX   MEDLINE=87241544; PubMed=3297057;
RA   Kahn P.H., Powell J.F., Beaumont A., Roques B.P., Mallet J.J.;
RT   "An antibody purified with a lambda GT11 fusion protein precipitates
RT   enkephalinase activity.";
RL   Biochem. Biophys. Res. Commun. 145:488-493(1987).
RN   [4]
RP   MUTAGENESIS.
RX   MEDLINE=88196403; PubMed=3162886;
RA   Devault A., Sales V., Nault C., Beaumont A., Roques B., Crine P.,
RA   Boileau G.;
RT   "Exploration of the catalytic site of endopeptidase 24.11 by site-
RT   directed mutagenesis. Histidine residues 583 and 587 are essential
RT   for catalysis.";
RL   FEBS Lett. 231:54-58(1988).
CC   -!- FUNCTION: THERMOLYSIN-LIKE SPECIFICITY, BUT IS ALMOST CONFINED ON
CC       ACTING ON POLYPEPTIDES OF UP TO 30 AMINO ACIDS. BIOLOGICALLY
CC       IMPORTANT IN THE DESTRUCTION OF OPIOID PEPTIDES SUCH AS MET-
CC       AND LEU-ENKEPHALINS BY CLEAVAGE OF A GLY-PHE BOND.
CC   -!- CATALYTIC ACTIVITY: Preferential cleavage at the amino group of
CC       hydrophobic residues in insulin, casein, hemoglobin, and a number
CC       of other proteins and polypeptides.
CC   -!- COFACTOR: BINDS 1 ZINC ION.
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein.
CC   -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M13.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X05338; CAA28950.1; -.
DR   EMBL; M16593; AAA53694.1; -.
DR   PIR; A29451; HYRBN.
DR   HSSP; P08473; 1DMT.
DR   MEROPS; M13.001; -.
DR   InterPro; IPR000718; Peptidase_M13.
DR   InterPro; IPR001230; Prenyl_site.
DR   InterPro; IPR000130; Zn_MTpeptdse.
DR   Pfam; PF01431; Peptidase_M13; 1.
DR   PRINTS; PR00786; NEPRILYSIN.
DR   PROSITE; PS00142; ZINC_PROTEASE; 1.
KW   Hydrolase; Metalloprotease; Zinc; Transmembrane; Glycoprotein;
KW   Signal-anchor.
FT   INIT_MET      0      0
FT   DOMAIN        1     27       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     28     50       SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT                                (POTENTIAL).
FT   DOMAIN       51    749       EXTRACELLULAR (POTENTIAL).
FT   DOMAIN       15     22       STOP-TRANSFER SEQUENCE (POTENTIAL).
FT   BINDING     102    102       FREE CARBOXYLATE OF SUBSTRATE
FT                                (BY SIMILARITY).
FT   METAL       583    583       ZINC (CATALYTIC).
FT   ACT_SITE    584    584       BY SIMILARITY.
FT   METAL       587    587       ZINC (CATALYTIC).
FT   METAL       646    646       ZINC (CATALYTIC) (BY SIMILARITY).
FT   ACT_SITE    650    650       PROTON DONOR (BY SIMILARITY).
FT   CARBOHYD    144    144       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    284    284       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    310    310       N-LINKED (GLCNAC. . .) (BY SIMILARITY).
FT   CARBOHYD    324    324       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    627    627       N-LINKED (GLCNAC. . .).
SQ   SEQUENCE   749 AA;  85450 MW;  E60B04357B0BABE9 CRC64;

 Query Match             32.1%;  Score 1270.5;  DB 1;  Length 749;
 Best Local Similarity   36.1%;  Pred. No. 6.9e-78;
 Matches  273;  Conservative  149;  Mismatches  290;  Indels   45;  Gaps   19;

Qy      13 KKANRGTRIALVVFVGGTLVLGTILFLVSQGLLSLQAKQE--YCLKPECIEAAAAILSKV 70
           ||  | | : : : |   |||  :| ::: :::| |  :   |  :|||::|| :: :
Db      18 KKKQRWTPLEISLSV---LVL--LLTVIAVTMIALYATYDDGICKSSDCIKSAARLIQNM 72

Qy      71 NLSVDPCDNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLEKSISRRRDTE 130
           : : :|| :||::|| ||:  | |||    |  :  ||  ::: ||::|::  :  |
Db      73 DATAEPCTDFFKYACGGWLKRNVIPETSSRYSNFDILRDELEVILKDVLQE--PKTEDIV 130

Qy     131 AIQKAKILYSSCMNEKAIEKADAKPLLHILRHSPFRWPVLESNIGPEGVWSE---RKFSL 187
           |:|||| || ||:|| ||:    :||| :|    : |||    |          | :    :|
Db     131 AVQKAKTLYRSCVNETAIDSRGGQPLLKLL-PDVYGWPVATQN------WEQTYGTSWSA 183

Qy     188 LQTLATFRGQYSNSVFIRLYVSPDDKASNEHILKLDQATLSLAVREDYLDNSTEAKSYRD 247
           :::|     |   | |  :|  ||| |  ||: :||  | |  | || : :   |
Db     184 EKSIAQLNSNYGKKVLINFFVGTDDKNSMNHIIHIDQPRLGLPSR-DYYECTGIYKEACT 242

Qy     248 ALYKFMVDTAVL------LGANSSRAEHDMKSVLRLEIKIAEIMIPHENRTSE-AMYNKM 300
           |   ||:  | |      | : ::   :|  |: || :||      |:|     :||||
Db     243 AYVDFMIAVAKLIRQEEGLPIDENQISVEMNKVMELEKEIANATTKSEDRNDPMLLYNKM 302

Qy     301 NISELSAMI------PQFDWLGYIKKVIDTRLYPHLKDISPSENVVVRVPQYFKDLFRIL 354
           ::::           | |  :  ::: |      :|   |:|||  |:|   |  ||
Db     303 TLAQIQNNFSLEINGKPFSWSNFTNEIMSTVNI----NIPNEEDVVVYAPEYLIKLKPIL 358

Qy     355 GSERKKTIANYLVWRMVYSRIPNLSRRFQYRWLEFSRVIQGTTTLLPQWDKCVNFIESAL 414
           :   |   || :   : :||| ::     | : : |||:    | :| |::   :
Db     359 TKYFPRDFQNLFSWRFIMDLVSSLSRTYKDSRNAFRKALYGTTSESATWRRCANYVNGNM 418

Qy     415 PYVVGKMFVDVYFQEDKKEMMEELVEGVRWAFIDMLEKENEWMDAGTKRKAKEKARAVLA 474
             ||:::|:  |  : | ::|:|:  :|  ||  |: :  |||| ||:||:||| |:
Db     419 ENAVGRLYVEAAFAGESKHVVEDLIAQIREVFIQTLD-DLTWMDAETKKKAEEKALAIKE 477

Qy     475 KVGYP-EFIMNDTHVNEDLKAIKFSEADYFGNVLQTRKYLAQSDFFWLRKAVPKTEWFTN 533
           ::||| : : ||  :| :   : : | :|| |::|  |:         ||: | | || |
Db     478 RIGYPDDIVSNDNKLNNEYLELNYKEDEYFENIIQNLKFSQSKQLKKLREKVDKDEWITG 537

Qy     534 PTTVNAFYSASTNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNGRKY 593
           |||||||:  ||| |||| || |||    :   ||:|| ||:::||| |||||:||| :
Db     538 AAIVNAFYSSGRNQIVFPAGILQPPFF-SAQQSNSLNYGGIGMVIGHEITHGFDDNGRNF 596

Qy     594 DKNGNLDPWWSTESEEKFKEKTKCMINQYSNYYWKKA-GLNVKGKRTLGENIADNGGLRE 652
           :|:|:|  ||: :|   |||:::||: || |: |  | | :: |  ||||||||||: :
Db     597 NKDGDLVDWWTQQSANNFKEQSQCMVYQYGNFSWDLAGGQHLNGINTLGENIADNGGIGQ 656

Qy     653 AFRAYRKWINDRRQGLEEPLLPGITFTNNQLFFLSYAHVRCNSYRPEAAREQVQIGAHSP 712
           |:|||: ::  :: | || |||||   : |||||:| | | :|||| |   ::   |||
Db     657 AYRAYQNYV--KKNG-EEKLLPGIDLNHKQLFFLNFAQVWCGTYRPEYAVNSIKTDVHSP 713

Qy     713 PQFRVNGAISNSEEFQKAFNCPPNSTMNRGMDSCRLW 749
             ||: |:: || || :|| || || ||     ||:|
Db     714 GNFRIIGSLQNSVEFSEAFQCPKNSYMN-PEKKCRVW 749


RESULT 5
NEP_RAT
ID   NEP_RAT        STANDARD;      PRT;   749 AA.
AC   P07861;
DT   01-AUG-1988 (Rel. 08, Created)
DT   01-AUG-1988 (Rel. 08, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Neprilysin (EC 3.4.24.11) (Neutral endopeptidase) (NEP)
DE   (Enkephalinase).
GN   MME.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX   MEDLINE=87213218; PubMed=3555489;
RA   Malfroy B., Schofield P.R., Kuang W.-J., Seeburg P.H., Mason A.J.,
RA   Henzel W.J.;
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RT   "Molecular cloning and amino acid sequence of rat enkephalinase.";
RL   Biochem. Biophys. Res. Commun. 144:59-66(1987).
RN   [2]
RP   ACTIVE SITE ARG-102.
RX   MEDLINE=89197908; PubMed=2703483;
RA   Bateman R.C. Jr., Jackson D., Slaughter C.A., Unnithan S., Chai Y.G.,
RA   Moomaw C., Hersh L.B.;
RT   "Identification of the active-site arginine in rat neutral
RT   endopeptidase 24.11 (enkephalinase) as arginine 102 and analysis of a
RT   glutamine 102 mutant.";
RL   J. Biol. Chem. 264:6151-6157(1989).
CC   -!- FUNCTION: THERMOLYSIN-LIKE SPECIFICITY, BUT IS ALMOST CONFINED ON
CC       ACTING ON POLYPEPTIDES OF UP TO 30 AMINO ACIDS. BIOLOGICALLY
CC       IMPORTANT IN THE DESTRUCTION OF OPIOID PEPTIDES SUCH AS MET-
CC       AND LEU-ENKEPHALINS BY CLEAVAGE OF A GLY-PHE BOND.
CC   -!- CATALYTIC ACTIVITY: Preferential cleavage at the amino group of
CC       hydrophobic residues in insulin, casein, hemoglobin, and a number
CC       of other proteins and polypeptides.
CC   -!- COFACTOR: BINDS 1 ZINC ION.
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein.
CC   -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M13.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M15944; AAA41116.1; -.
DR   PIR; A29295; HYRTN.
DR   HSSP; P08473; 1DMT.
DR   MEROPS; M13.001; -.
DR   InterPro; IPR000718; Peptidase_M13.
DR   InterPro; IPR001230; Prenyl_site.
DR   InterPro; IPR000130; Zn_MTpeptdse.
DR   Pfam; PF01431; Peptidase_M13; 1.
DR   PRINTS; PR00786; NEPRILYSIN.
DR   PROSITE; PS00142; ZINC_PROTEASE; 1.
KW   Hydrolase; Metalloprotease; Zinc; Transmembrane; Glycoprotein;
KW   Signal-anchor.
FT   INIT_MET      0      0
FT   DOMAIN        1     27       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     28     50       SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT                                (POTENTIAL).
FT   DOMAIN       51    749       EXTRACELLULAR (POTENTIAL).
FT   DOMAIN       15     22       STOP-TRANSFER SEQUENCE (POTENTIAL).
FT   BINDING     102    102       FREE CARBOXYLATE OF SUBSTRATE.
FT   METAL       583    583       ZINC (CATALYTIC) (BY SIMILARITY).
FT   ACT_SITE    584    584       BY SIMILARITY.
FT   METAL       587    587       ZINC (CATALYTIC) (BY SIMILARITY).
FT   METAL       646    646       ZINC (CATALYTIC) (BY SIMILARITY).
FT   ACT_SITE    650    650       PROTON DONOR (BY SIMILARITY).
FT   CARBOHYD    144    144       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    210    210       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    284    284       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    310    310       N-LINKED (GLCNAC. . .).
FT   CARBOHYD    324    324       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    627    627       N-LINKED (GLCNAC. . .) (BY SIMILARITY).
SQ   SEQUENCE   749 AA;  85663 MW;  89B0EC50A9016A47 CRC64;

  Query Match             31.9%;  Score 1263.5;  DB 1;  Length 749;
  Best Local Similarity   35.7%;  Pred. No. 2e-77;
  Matches  270;  Conservative  151;  Mismatches  291;  Indels   45;  Gaps   19;

Qy      13 KKANRGTRIALVVFVGGTLVLGTILFLVSQGLLSLQAKQE--YCLKPECIEAAAAILSKV 70
           ||  | | : : : |   |||  :| :::  :::| |  :   |   :||::|| ::  :
Db      18 KKKQRWTPLEISLSV---LVL--LLTIIAVTMIALYATYDDGICKSSDCIKSAARLIQNM 72

Qy      71 NLSVDPCDNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLEKSISRRRDTE 130
           : | :|| :||::|| ||:  | |||    |  :  ||  ::: ||::|::   :  |
Db      73 DASAEPCTDFFKYACGGWLKRNVIPETSSRYSNFDILRDELEVILKDVLQE--PKTEDIV 130

Qy     131 AIQKAKILYSSCMNEKAIEKADAKPLLHILRHSPFRWPVLESNIGPEGVWSE---RKFSL 187
           |:|||| || ||:|| ||:    :||| :|    : |||   |      | :     ::
Db     131 AVQKAKTLYRSCINESAIDSRGGQPLLTLL-PDIYGWPVASQN------WEQTYGTSWTA 183

Qy     188 LQTLATFRGQYSNSVFIRLYVSPDDKASNEHILKLDQATLSLAVREDYLDNSTEAKSYRD 247
           :::|    :|   | |  :|  ||| | :||:  ||  | |  | || : :   |
Db     184 EKSIAQLNSKYGKKVLINFFVGTDDKNSTQHIIHFDQPRLGLPSR-DYYECTGIYKEACT 242

Qy     248 ALYKFMVDTAVL------LGANSSRAEHDMKSVLRLEIKIAEIMIPHENRTSE-AMYNKM 300
           |   ||:  | |       |  : ::   :|  |: || :||      |:|      :||||
Db     243 AYVDFMISVARLIRQEQRLPIDENQLSLEMNKVMELEKEIANATTKPEDRNDPMLLYNKM 302

Qy     301 NISELSAMI------PQFDWLGYIKKVIDTRLYPHLKDISPSENVVVRVPQYFKDLFRIL 354
           :::|              | |  :  ::: |       :|   | |||  |:|   |  ||
Db     303 TLAKLQNNFSLEINGKPFSWSNFTNEIMSTVNI----NIQNEEEVVVYAPEYLTKLKPIL 358

Qy     355 GSERKKTIANYLVWRMVYSRIPNLSRRFQYRWLEFSRVIQGTTTLLPQWDKCVNFIESAL 414
           : : | : || :   : :||| ::     | : : |||:     | :| |::   :
Db     359 TKYSPRDLQNLMSWRFIMDLVSSLSRNYKESRNAFRKALYGTTSETATWRRCANYVNGNM 418

Qy     415 PYVVGKMFVDVYFQEDKKEMMEELVEGVRWAFIDMLEKENEWMDAGTKRKAKEKARAVLA 474
           ||:::|:  |  : | ::|:|:  :|  ||  |: :  |||| ||:||:||| |:
Db     419 ENAVGRLYVEAAFAGESKHVVEDLIAQIREVFIQTLD-DLTWMDAETKKKAEEKALAIKE 477

Qy     475 KVGYP-EFIMNDTHVNEDLKAIKFSEADYFGNVLQTRKYLAQSDFFWLRKAVPKTEWFTN 533
           ::||| : | |:  :| :   : : | :|| |::|  |:          ||: | | || :
Db     478 RIGYPDDIISNENKLNNEYLELNYKEEEYFENIIQNLKFSQSKQLKKLREKVDKDEWISG 537

Qy     534 PTTVNAFYSASTNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNGRKY 593
           ||||||:  ||| |||| || |||       ||:|| ||:::||| |||||:||| :
Db     538 AAVVNAFYSSGRNQIVFPAGILQPPFF-SARQSNSLNYGGIGMVIGHEITHGFDDNGRNF 596

Qy     594 DKNGNLDPWWSTESEEKFKEKTKCMINQYSNYYWKKA-GLNVKGKRTLGENIADNGGLRE 652
           :|:|:|  ||: :|   ||::::||: || |: |  | | :: |  ||||||||||: :
Db     597 NKDGDLVDWWTQQSANNFKDQSQCMVYQYGNFTWDLAGGQHLNGINTLGENIADNGGIGQ 656

Qy     653 AFRAYRKWINDRRQGLEEPLLPGITFTNNQLFFLSYAHVRCNSYRPEAARE-QVQIGAHSP 712
           |:|||: ::  :: | || ||||:   : |||||::| | | :|||| |   ::   |||
Db     657 AYRAYQNYV--KKNG-EEKLLPGLDLNHKQLFFLNFAQVWCGTYRPEYAVNSIKTDVHSP 713

Qy     713 PQFRVNGAISNSEEFQKAFNCPPNSTMNRGMDSCRLW 749
           ||: | : || ||  ||:|  || ||     ||:|
Db     714 GNFRIIGTLQNSAEFADAFHCRKNSYMNPER-KCRVW 749


RESULT 6
ECE1_CAVPO
ID   ECE1_CAVPO     STANDARD;      PRT;   754 AA.
AC   P97739;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Endothelin-converting enzyme 1 (EC 3.4.24.71) (ECE-1).
GN   ECE1.
OS   Cavia porcellus (Guinea pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX   NCBI_TaxID=10141;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96192242; PubMed=8624482;
RA   Shima H., Yamanouchi M., Omori K., Sugiura M., Kawashima K.,
RA   Sato T.;
RT   "Endothelin-1 production and endothelin converting enzyme expression
RT   by guinea pig airway epithelial cells.";
RL   Biochem. Mol. Biol. Int. 37:1001-1010(1995).
CC   -!- FUNCTION: CONVERTS BIG ENDOTHELIN-1 TO ENDOTHELIN-1.
CC   -!- CATALYTIC ACTIVITY: Forms endothelin 1 by cleavage of the 21-
CC       Trp-|-Val-22 bond in the precursor.
CC   -!- ENZYME REGULATION: INHIBITED BY PHOSPHORAMIDON (BY SIMILARITY).
CC   -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein.
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CC   -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M13.
CC   ---------------------------------------------------------------------
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CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   use by non-profit institutions as long as its content is in no way
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; S82653; AAB46734.1; -.
DR   HSSP; P08473; 1DMT.
DR   MEROPS; M13.002; -.
DR   InterPro; IPR000718; Peptidase_M13.
DR   InterPro; IPR000130; Zn_MTpeptdse.
DR   Pfam; PF01431; Peptidase_M13; 1.
DR   PRINTS; PR00786; NEPRILYSIN.
DR   PROSITE; PS00142; ZINC_PROTEASE; 1.
KW   Hydrolase; Metalloprotease; Zinc; Glycoprotein; Transmembrane;
KW   Signal-anchor.
FT   DOMAIN        1     52       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     53     73       SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT                                 (POTENTIAL).
FT   DOMAIN       74    754       EXTRACELLULAR (POTENTIAL).
FT   METAL       591    591       ZINC (CATALYTIC) (BY SIMILARITY).
FT   ACT_SITE    592    592       BY SIMILARITY.
FT   METAL       595    595       ZINC (CATALYTIC) (BY SIMILARITY).
FT   METAL       651    651       ZINC (CATALYTIC) (BY SIMILARITY).
FT   ACT_SITE    655    655       PROTON DONOR (BY SIMILARITY).
FT   CARBOHYD    150    150       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    171    171       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    194    194       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    254    254       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    300    300       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    346    346       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    367    367       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    523    523       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    616    616       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    635    635       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   754 AA;  85772 MW;  F0646C57FF2BA8A0 CRC64;

  Query Match           31.9%;  Score 1262.5;  DB 1;  Length 754;
  Best Local Similarity 38.0%;  Pred. No. 2.4e-77;
  Matches  284;  Conservative  128;  Mismatches  270;  Indels   65;  Gaps   22;

Qy      23 LVVFVGGTLVLGTILFLVSQGLLSLQAKQEYCLKPECIEAAAAILSKVNLSVDPCDNFFR 82
           |:| |   |  | : |:          ||   |:  ::||: :| :|||| :||
Db      53 LIVLV-ALLAAGLVACLTALGIQYRTRTPPVCLSEACVSVTSSILNSMNPTVDPCQDFFS 111

Qy      83 FACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLEKSISRRRDTEAIQKAKILYSSC 142
           :|| |||  ||:|:   :| :  |  :   :| ||| | :    :|| :||:: | :|
Db     112 YACGGWIKANPVPDGHSRWGAFSNLWEHNQAIIKHLLENSTA--SVSEAERKAQVYYRAC 169

Qy     143 MNEKAIEKADAKPLLHILRHSPFRWPVLESNIGPEGVWSERKFSLLQTLATFRGQYSNSV 202
           |||  ||:  ||||: ::      | :          | |::  |    ||      |  |
Db     170 MNETRIEELRAKPLMELIEKLG-GWNI-------TGPWAKDNFQ--DTLQVVTAHYRTSP 219

Qy     203 FIRLYVSPDDKASNEHILKLDQATLSLAVREDYLDNSTEAKSYRDALYKFMVDTAVLLGA 262
           |  :||| | | || ::: :||: | |  |: || | || :   :    :||   |||
Db     220 FFSVYVSADSKNSNRNVIHVDQSGLGLPSRDYYL-NKTENEKVLNGYLNYMVQLGKLLGG 278

Qy     263 ---NSSRAEHDMKSVLRLEIKIAEIMIPHENRTSEAM-YNKMNISELSAMIPQFDWLGYI 318
              |: ||:  |: :|  |  :| | || | |  | : |:|:  :||  : |  :|| :
Db     279 GDENAIRAQ--MQQILDFETALANITIPQEKRRDEELIYHKVTAAELQTLAPAINWLPF- 335

Qy     319 KKVIDTRLYPHLKDISPSENVVVRVPQYFKDLFRILGSERKKTIANYLVWRMVYSRIPNL 378
           ::|  ||   :|: || :||   :| : :  :: :  |  : ||::| :|      |
Db     336 ---LNTIFYP--VEINESEPIVVYDKEYLEQVSTLINTTDKCLLNNYMIWNLVRKTSSFL 390

Qy     379 SRRFQYRWLEFSRVIQGT-TTLLPQWDKCVNFIESALPYVVGKMFVDVYFQEDKKEMMEE 437
           :|||    :|  |: ||  | ||:|  ||:  |: | : :| |||   | || | :  |
Db     391 DQRFQDADEKFMEVMYGTKKTCLPRWKFCVSDTENNLGFGLGPMFVKATFAEDSKNIASE 450

Qy     438 LVEGVRWAFIDMLEKENEWMDAGTKRKAKEKARAVLAKVGYPEFIM---------NDTHV 488
           ::  :: || : |    :|||  |:: ||||| |:   :||| |||          ||
Db     451 IILEIKKAFEESL-STLKWMDEDTRKSAKEKADAIYNMIGYPNFIMDPKELDKVFNDYTA 509

Qy     489 NEDLKAIKFSEADYFGNVLQTRKYLAQSDFFW------LRKAVPKTEWFTNPTTVNAFYS 542
           ||          || | ::        :| |      ||||  : :|   |  |||:||
Db     510 VPDL---------YFENAMRF------FNFSWRVTAEQLRKAPNRDQWSMTPPMVNAYYS 554

Qy     543 ASTNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNGRKYDKNGNLDPW 602
           : |:| |||| |  ||:  :  |:::|::| |||:|||| || ||: ||:|||:||| ||
Db     555 PTKNEIVFPAGILPAPFYTRSS-PKALNFGGIGVVVGHELTHAFDDQGREYDKDGNLRPW 613

Qy     603 WSTESEEKFKEKTKCMINQYSNYYWKKAGLNVKGKRTLGENIADNGGLREAFRAYRKWIN 662
           |   | | ||::|:||: |||||      |  | |: ||||||||||||: |:|||: |:
Db     614 WKNSSVEAFKQQTECMVEQYSNY--SVNGEPVNGRHTLGENIADNGGLKAAYRAYQNWV- 670

Qy     663 DRRQGLEEPLLPGITFTNNQLFFLSYAHVRCNSYRPEAAREQVQIGAHSPPQFRVNGAIS 722
           :: | ||  || :  ||||||||| :| | |:   ||:: | :    ||| :||| |::|
Db     671 -KKNGAEE-TLPTLGLTNNQLFFLGFAQVWCSVRTPESSHEGLITDPHSPSRFRVIGSLS 728

Qy     723 NSEEFQKAFNCPPNSTMNRGMDSCRLW 749
           ||:|| : | ||| | ||      | :|
Db     729 NSKEFSEHFQCPPGSPMN-PRHKCEVW 754


RESULT 7
NEP_MOUSE
ID   NEP_MOUSE       STANDARD;       PRT;   749 AA.
AC   Q61391;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Neprilysin (EC 3.4.24.11) (Neutral endopeptidase) (NEP)
DE   (Enkephalinase) (Neutral endopeptidase 24.11) (CD10).
GN   MME.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c;
RX   MEDLINE=92242908; PubMed=1374101;
RA   Chen C.Y., Salles G., Seldin M.F., Kister A.E., Reinher E.L.,
RA   Shipp M.A.;
RT   "Murine common acute lymphoblastic leukemia antigen (CD10 neutral
RT   endopeptidase 24.11). Molecular characterization, chromosomal
RT   localization, and modeling of the active site.";
RL   J. Immunol. 148:2817-2825(1992).
CC   -!- FUNCTION: THERMOLYSIN-LIKE SPECIFICITY, BUT IS ALMOST CONFINED ON
CC       ACTING ON POLYPEPTIDES OF UP TO 30 AMINO ACIDS. BIOLOGICALLY
CC       IMPORTANT IN THE DESTRUCTION OF OPIOID PEPTIDES SUCH AS MET-
CC       AND LEU-ENKEPHALINS BY CLEAVAGE OF A GLY-PHE BOND.
CC   -!- CATALYTIC ACTIVITY: Preferential cleavage at the amino group of
CC       hydrophobic residues in insulin, casein, hemoglobin, and a number
CC       of other proteins and polypeptides.
CC   -!- COFACTOR: BINDS 1 ZINC ION.
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein.
CC   -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M13.
CC   ---------------------------------------------------------------------
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CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M81591; AAA37386.1; -.
DR   HSSP; P08473; 1DMT.
DR   MEROPS; M13.001; -.
DR   MGD; MGI:97004; Mme.
DR   InterPro; IPR000718; Peptidase_M13.
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DR   InterPro; IPR001230; Prenyl_site.
DR   InterPro; IPR000130; Zn_MTpeptdse.
DR   Pfam; PF01431; Peptidase_M13; 1.
DR   PRINTS; PR00786; NEPRILYSIN.
DR   PROSITE; PS00142; ZINC_PROTEASE; 1.
KW   Hydrolase; Metalloprotease; Zinc; Transmembrane; Glycoprotein;
KW   Signal-anchor.
FT   INIT_MET      0      0       BY SIMILARITY.
FT   DOMAIN        1     27       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     28     50       SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT                                (POTENTIAL).
FT   DOMAIN       51    749       EXTRACELLULAR (POTENTIAL).
FT   DOMAIN       15     22       STOP-TRANSFER SEQUENCE (POTENTIAL).
FT   BINDING     102    102       FREE CARBOXYLATE OF SUBSTRATE
FT                                (BY SIMILARITY).
FT   METAL       583    583       ZINC (CATALYTIC) (BY SIMILARITY).
FT   ACT_SITE    584    584       BY SIMILARITY.
FT   METAL       587    587       ZINC (CATALYTIC) (BY SIMILARITY).
FT   METAL       646    646       ZINC (CATALYTIC) (BY SIMILARITY).
FT   ACT_SITE    650    650       PROTON DONOR (BY SIMILARITY).
FT   CARBOHYD    144    144       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    210    210       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    284    284       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    310    310       N-LINKED (GLCNAC. . .) (BY SIMILARITY).
FT   CARBOHYD    324    324       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    627    627       N-LINKED (GLCNAC. . .) (BY SIMILARITY).
SQ   SEQUENCE   749 AA;  85509 MW;  5FE1AC6685FDEE30 CRC64;

  Query Match           31.8%;  Score 1259.5;  DB 1;  Length 749;
  Best Local Similarity  35.8%;  Pred. No. 3.8e-77;
  Matches  272;  Conservative  149;  Mismatches  289;  Indels   49;  Gaps   20;

Qy      13 KKANRGT--RIALVVFVGGTLVLGTILFLVSQGLLSLQAKQE--YCLKPECIEAAAAILS 68
Db      18 KKKQRWTPLEISLSVLV----LLXTIIAVT---MIALYATYDDGICKSSDCIKSAARLIQ 70

Qy      69 KVNLSVDPCDNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLEKSISRRRD 128
Db      71 NMDASVEPCTDFFKYACGGWLKRNVIPETSSRYSNFDILRDELEVILKDVLQE--PKTED 128

Qy     129 TEAIQKAKILYSSCMNEKAIEKADAKPLLHILRHSPFRWPVLESNIGPEGVWSE---RKF 185
Db     129 IVAVQKAKTLYRSCINESAIDSRGGQPLLKLL-PDIYGWPVASDN------WDQTYGTSW 181

Qy     186 SLLQTLATFRGQYSNSVFIRLYVSPDDKASNEHILKLDQATLSLAVREDYLDNSTEAKSY 245
Db     182 TAEKSIAQLNSKYGKKVLINFFVGTDDKNSTQHIIHFDQPRLGLPSR-GYYECTGIYKEA 240

Qy     246 RDALYKFMVDTAVL------LGANSSRAEHDMKSVLRLEIKIAEIMIPHENRTSE-AMYN 298
Db     241 CTAYVDFMISVARLIRQEQSLPIDENQLSLEMNKVMELEKEIANATTKPEDRNDPMLLYN 300

Qy     299 KMNISELSAMI------PQFDWLGYIKKVIDTRLYPHLKDISPSENVVVRVPQYFKDLFR 352
Db     301 KMTLAKLQNNFSLEVNGKSFSWSNFTNEIMSTVNI----NIQNEEEVVVYAPEYLTKLKP 356

Qy     353 ILGSERKKTIANYLVWRMVYSRIPNLSRRFQYRWLEFSRVIQGTTTLLPQWDKCVNFIES 412
Db     357 ILTKYSPRDLQNLMSWRFIMDLVSSLSRNYKESRNAFRKALYGTTSETATWRRCANYVNG 416

Qy     413 ALPYVVGKMFVDVYFQEDKKEMMEELVEGVRWAFIDMLEKENEWMDAGTKRKAKEKARAV 472
Db     417 NMENAVGRLYVEAAFAGESKHVVEDLIAQIREVFIQTLD-DLTWMDAETKKKAEEKALAI 475

Qy     473 LAKVGYP-EFIMNDTHVNEDLKAIKFSEADYFGNVLQTRKYLAQSDFFWLRKAVPKTEWF 531
Db     476 KERIGYPDDIISNENKLNNEYLELNYREDEYFENIIQNLKFSQSKQLKKLREKVDKDEWI 535

Qy     532 TNPTTVNAFYSASTNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNGR 591
Db     536 SGAAVVNAFYSSGRNQIVFPAGILQPPFF-SAQQSNSLNYGGIGMVIGHEITHGFDDNGR 594

Qy     592 KYDKNGNLDPWWSTESEEKFKEKTKCMINQYSNYYWKKA-GLNVKGKRTLGENIADNGGL 650
Db     595 NFNKDGDLVDWWTQQSANNFKDQSQCMVYQYGNFSWDLAGGQHLNGINTLGENIADNGGI 654

Qy     651 REAFRAYRKWINDRRQGLEEPLLPGITFTNNQLFFLSYAHVRCNSYRPEAAREQVQIGAH 710
Db     655 GQAYRAYQNYV--KKNG-EEKLLPGLDLNHKQLFFLNFAQVWCGTYRPEYAVNSIKTDVH 711

Qy     711 SPPQFRVNGAISNSEEFQKAFNCPPNSTMNRGMDSCRLW 749
Db     712 SPGNFRIIGTLQNSAEFADAFHCRKNSYMNPER-KCRVW 749


RESULT 8
ECE1_HUMAN
ID   ECE1_HUMAN     STANDARD;      PRT;   770 AA.
AC   P42892; Q14217; Q9UJQ6; Q9UPF4; Q9UPM4; Q9Y501;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Endothelin-converting enzyme 1 (EC 3.4.24.71) (ECE-1).
GN   ECE1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE OF 7-770 FROM N.A. (ISOFORM B).
RC   TISSUE=Placenta;
RX   MEDLINE=95104423; PubMed=7805846;
RA   Schmidt M., Kroeger B., Jacob E., Seulberger H., Subkowski T.,
RA   Otter R., Meyer T., Schmalzing G., Hillen H.;
RT   "Molecular characterization of human and bovine endothelin converting
RT   enzyme (ECE-1).";
RL   FEBS Lett. 356:238-243(1994).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM B).
RX   MEDLINE=95209687; PubMed=7695628;
RA   Yorimitsu K., Moroi K., Inagaki N., Saito T., Masuda Y.,
RA   Masaki T., Seino S., Kimura S.;
RT   "Cloning and sequencing of a human endothelin converting enzyme in
RT   renal adenocarcinoma (ACHN) cells producing endothelin-2.";
RL   Biochem. Biophys. Res. Commun. 208:721-727(1995).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORMS A AND B).
RC   TISSUE=Placenta;
RX   MEDLINE=96102029; PubMed=8530372;
RA   Valdenaire O., Rohrbacher E., Mattei M.-G.;
RT   "Organization of the gene encoding the human endothelin-converting
RT   enzyme (ECE-1).";
RL   J. Biol. Chem. 270:29794-29798(1995).
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORM A).
RX   MEDLINE=95169128; PubMed=7864876;
RA   Shimada K., Matsushita Y., Wakabayashi K., Takahashi M., Matsubara A.,
RA   Iijima Y., Tanzawa K.;
RT   "Cloning and functional expression of human endothelin-converting
RT   enzyme cDNA.";
RL   Biochem. Biophys. Res. Commun. 207:807-812(1995).
RN   [5]
RP   SEQUENCE FROM N.A. (ISOFORM C).
RC   TISSUE=Umbilical vein endothelial cells;
RA   Takayanagi R.;
RT   "Human endothelin-converting enzyme-1c.";
RL   Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   SEQUENCE FROM N.A. (ISOFORM B).
RA   Pearce A.;
RL   Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
RN   [7]
RP   SEQUENCE OF 1-132 FROM N.A. (ISOFORM D), AND TISSUE SPECIFICITY.
RX   MEDLINE=99421637; PubMed=10491078;
RA   Valdenaire O., Lepailleur-Enouf D., Egidy G., Thouard A., Barret A.,
RA   Vranckx R., Tougard C., Michel J.-B.;
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RT   "A fourth isoform of endothelin-converting enzyme (ECE-1) is generated
RT   from an additional promoter.";
RL   Eur. J. Biochem. 264:341-349(1999).
RN   [8]
RP   SEQUENCE OF 1-103 FROM N.A. (ISOFORM C), FUNCTION, AND TISSUE
RP   SPECIFICITY.
RC   TISSUE=Umbilical vein endothelial cells;
RX   MEDLINE=98060745; PubMed=9396733;
RA   Schweizer A., Valdenaire O., Nelboeck P., Deuschle U.,
RA   Dumas Milne Edwards J.B., Stumpf J.G., Loeffler B.-M.;
RT   "Human endothelin-converting enzyme (ECE-1): three isoforms with
RT   distinct subcellular localizations.";
RL   Biochem. J. 328:871-877(1997).
RN   [9]
RP   SEQUENCE OF 1-46 FROM N.A. (ISOFORM B).
RA   Bagguley C.;
RL   Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
RN   [10]
RP   SEQUENCE OF 713-770 FROM N.A.
RA   Flowers M.A., Tai S.C., Baluyut C.A., Cheung A.H., Kau C.L.,
RA   Wong G.K.T., Marsden P.A.;
RT   "Characterization of the human endothelin converting enzyme-1 gene
RT   (ECE-1): genomic structure and chromosomal localization.";
RL   Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: CONVERTS BIG ENDOTHELIN-1 TO ENDOTHELIN-1.
CC   -!- CATALYTIC ACTIVITY: Forms endothelin 1 by cleavage of the 21-
CC       Trp-|-Val-22 bond in the precursor.
CC   -!- ENZYME REGULATION: INHIBITED BY PHOSPHORAMIDON.
CC   -!- SUBUNIT: HOMODIMER.
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein.
CC   -!- ALTERNATIVE PRODUCTS: 4 ISOFORMS; A, B (SHOWN HERE), C AND D; ARE
CC       PRODUCED BY ALTERNATIVE SPLICING.
CC   -!- TISSUE SPECIFICITY: ALL ISOFORMS ARE EXPRESSED IN UMBLICAL VEIN
CC       ENDOTHELIAL CELLS, POLYNUCLEAR NEUTROPHILS, FIBROBLASTS, ATRIUM
CC       CARDIOMYOCYTES AND VENTRICLES. ISOFORMS A, B AND C ARE ALSO
CC       EXPRESSED IN PLACENTA, LUNG, HEART, ADRENAL GLAND AND
CC       PHAEOCHROMOCYTOMA; ISOFORMS A AND C IN LIVER, TESTIS AND SMALL
CC       INTESTINE; ISOFORM B, C AND D IN ENDOTHELIAL CELLS AND UMBLICAL
CC       VEIN SMOOTH MUSCLE CELLS; ISOFORMS C AND D IN SAPHENOUS VEIN
CC       CELLS, AND ISOFORM C IN KIDNEY.
CC   -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M13.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; Z35307; CAA84548.1; ALT_INIT.
DR   EMBL; D49471; BAA08442.1; -.
DR   EMBL; X91922; CAA63015.1; -.
DR   EMBL; X91923; CAA63015.1; JOINED.
DR   EMBL; X91924; CAA63015.1; JOINED.
DR   EMBL; X91925; CAA63015.1; JOINED.
DR   EMBL; X91926; CAA63015.1; JOINED.
DR   EMBL; X91927; CAA63015.1; JOINED.
DR   EMBL; X91928; CAA63015.1; JOINED.
DR   EMBL; X91929; CAA63015.1; JOINED.
DR   EMBL; X91930; CAA63015.1; JOINED.
DR   EMBL; X91931; CAA63015.1; JOINED.
DR   EMBL; X91932; CAA63015.1; JOINED.
DR   EMBL; X91933; CAA63015.1; JOINED.
DR   EMBL; X91934; CAA63015.1; JOINED.
DR   EMBL; X91935; CAA63015.1; JOINED.
DR   EMBL; X91936; CAA63015.1; JOINED.
DR   EMBL; X91937; CAA63015.1; JOINED.
DR   EMBL; X91938; CAA63015.1; JOINED.
DR   EMBL; X91939; CAA63015.1; JOINED.
DR   EMBL; X91923; CAA63016.1; -.
DR   EMBL; X91924; CAA63016.1; JOINED.
DR   EMBL; X91925; CAA63016.1; JOINED.
DR   EMBL; X91926; CAA63016.1; JOINED.
DR   EMBL; X91927; CAA63016.1; JOINED.
DR   EMBL; X91928; CAA63016.1; JOINED.
DR   EMBL; X91929; CAA63016.1; JOINED.
DR   EMBL; X91930; CAA63016.1; JOINED.
DR   EMBL; X91931; CAA63016.1; JOINED.
DR   EMBL; X91932; CAA63016.1; JOINED.
DR   EMBL; X91933; CAA63016.1; JOINED.
DR   EMBL; X91934; CAA63016.1; JOINED.
DR   EMBL; X91935; CAA63016.1; JOINED.
DR   EMBL; X91936; CAA63016.1; JOINED.
DR   EMBL; X91937; CAA63016.1; JOINED.
DR   EMBL; X91938; CAA63016.1; JOINED.
DR   EMBL; X91939; CAA63016.1; JOINED.
DR   EMBL; D43698; BAA07800.1; -.
DR   EMBL; AB031742; BAA83687.1; -.
DR   EMBL; AL031005; CAA19767.1; -.
DR   EMBL; AJ130828; CAB46443.1; -.
DR   EMBL; X98272; CAA66922.1; -.
DR   EMBL; AL031728; CAB52285.1; -.
DR   EMBL; AF018034; AAD21221.1; -.
DR   HSSP; P08473; 1DMT.
DR   MEROPS; M13.002; -.
DR   Genew; HGNC:3146; ECE1.
DR   MIM; 600423; -.
DR   InterPro; IPR000718; Peptidase_M13.
DR   InterPro; IPR000130; Zn_MTpeptdse.
DR   Pfam; PF01431; Peptidase_M13; 1.
DR   PRINTS; PR00786; NEPRILYSIN.
DR   PROSITE; PS00142; ZINC_PROTEASE; 1.
KW   Hydrolase; Metalloprotease; Zinc; Glycoprotein; Transmembrane;
KW   Signal-anchor; Alternative splicing; Polymorphism.
FT   DOMAIN        1     68       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     69     89       SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT                                (POTENTIAL).
FT   DOMAIN       90    770       EXTRACELLULAR (POTENTIAL).
FT   METAL       607    607       ZINC (CATALYTIC) (BY SIMILARITY).
FT   ACT_SITE    608    608       BY SIMILARITY.
FT   METAL       611    611       ZINC (CATALYTIC) (BY SIMILARITY).
FT   METAL       667    667       ZINC (CATALYTIC) (BY SIMILARITY).
FT   ACT_SITE    671    671       PROTON DONOR (BY SIMILARITY).
FT   CARBOHYD    166    166       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    187    187       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    210    210       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    270    270       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    316    316       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    362    362       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    383    383       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    539    539       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    632    632       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    651    651       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC      1     44       MRGVWPPPVSALLSALGMSTYKRATLDEEDLVDSLSEGDAY
FT                                PNG -> MPLQGLGLQRNPFLQGKRGPGLTSSPPLLPPS
FT                                (IN ISOFORM A).
FT   VARSPLIC      1     17       MRGVWPPPVSALLSALG -> MEALRESVLHLALQ (IN
FT                                ISOFORM D).
FT   VARSPLIC      1     17       MRGVWPPPVSALLSALG -> M (IN ISOFORM C).
FT   VARIANT     341    341       T -> I (IN DBSNP:1076669).
FT                                /FTId=VAR_011972.
SQ   SEQUENCE   770 AA;  87163 MW;  DD88A59748B22F80 CRC64;

  Query Match             31.8%;  Score 1257;  DB 1;  Length 770;
  Best Local Similarity   37.6%;  Pred. No. 5.8e-77;
  Matches  281;  Conservative  126;  Mismatches  276;  Indels   64;  Gaps   21;

Qy      21 IALVVFVGGTLVLGTILFLVSQGLLSLQAKQEYCLKPECIEAAAAILSKVNLSVDPCDNF 80
           : |||     |  | :  | : |:          ||   |:   ::||| :: :|||| :|
Db      70 VVLVVL----LAAGLVACLAALGIQYQTRSPSVCLSEACVSVTSSILSSMDPTVDPCHDF 125

Qy      81 FRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLEKSISRRRDTEAIQKAKILYS 140
           | :|| |||  ||:|:    :| :  |  :    :| ||| | :    :|| :||:: |
Db     126 FSYACGGWIKANPVPDGHSRWGTFSNLWEHNQAIIKHLLENSTA--SVSEAERKAQVYYR 183
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Qy    141 SCMNEKAIEKADAKPLLHILRHSPFRWPVLESNIGPEGVWSERKFSLLQTLATFRGQYSN 200
          :||||  ||:  ||||: ::      | :        | |::  |    ||      |
Db    184 ACMNETRIEELRAKPLMELIERLG-GWNI-------TGPWAKDNFQ--DTLQVVTAHYRT 233

Qy    201 SVFIRLYVSPDDKASNEHILKLDQATLSLAVREDYLDNSTEAKSYRDALYKFMVDTAVLL 260
          | |  :||| | | || ::::::||: | |  |: || | || :          :||    ||
Db    234 SPFFSVYVSADSKNSNSNVIQVDQSGLGLPSRDYYL-NKTENEKVLTGYLNYMVQLGKLL 292

Qy    261 GANSSRA-EHDMKSVLRLEIKIAEIMIPHENRTSEAM-YNKMNISELSAMIPQFDWLGYI 318
          |      |    |: :|  |  :| | || | |  | : |:|:  :||  : |  :|| :
Db    293 GGGDEEAIRPQMQQILDFETALANITIPQEKRRDEELIYHKVTAAELQTLAPAINWLPF- 351

Qy    319 KKVIDTRLYPHLKDISPSENVVVRVPQYFKDLFRILGSERKKTIANYLVWRMVYSRIPNL 378
             ::|  ||   :|: || :||   :| : :  :: :  :  : ||::| :|       |
Db    352 ---LNTIFYP--VEINESEPIVVYDKEYLEQISTLINTTDRCLLNNYMIWNLVRKTSSFL 406

Qy    379 SRRFQYRWLEFSRVIQGT-TTLLPQWDKCVNFIESALPYVVGKMFVDVYFQEDKKEMMEE 437
          :|||    :|  |: || | ||:|  ||:  |: | : :| |||    | || | :  |
Db    407 DQRFQDADEKFMEVMYGTKKTCLPRWKFCVSDTENNLGFALGPMFVKATFAEDSKSIATE 466

Qy    438 LVEGVRWAFIDMLEKENEWMDAGTKRKAKEKARAVLAKVGYPEFIM---------NDTHV 488
          ::  :: || : |    :|||  |:: ||||| |:   :||| |||          ||
Db    467 IILEIKKAFEESL-STLKWMDEETRKSAKEKADAIYNMIGYPNFIMDPKELDKVFNDYTA 525

Qy    489 NEDLKAIKFSEADYFGNVLQTRKYLAQSDFFW------LRKAVPKTEWFTNPTTVNAFYS 542
            ||         || | ::       :| |      ||||  : :|   |  |||:||
Db    526 VPDL---------YFENAMRF------FNFSWRVTADQLRKAPNRDQWSMTPPMVNAYYS 570

Qy    543 ASTNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNGRKYDKNGNLDPW 602
          : |:| |||| || ||:  :  |::|:::| |||:|||| || ||: ||:|||:||| ||
Db    571 PTKNEIVFPAGILQAPFYTRSS-PKALNFGGIGVVVGHELTHAFDDQGREYDKDGNLRPW 629

Qy    603 WSTESEEKFKEKTKCMINQYSNYYWKKAGLNVKGKRTLGENIADNGGLREAFRAYRKWIN 662
          |   | | || :|:||: |||||     |  | |: ||||||||||||: |:|||: |:
Db    630 WKNSSVEAFKRQTECMVEQYSNY--SVNGEPVNGRHTLGENIADNGGLKAAYRAYQNWV- 686

Qy    663 DRRQGLEEPLLPGITFTNNQLFFLSYAHVRCNSYRPEAAREQVQIGAHSPPQFRVNGAIS 722
          :: | |   || :  |||||||| :| | |:   ||:: | :    ||| :||| |::|
Db    687 -KKNGAEHS-LPTLGLTNNQLFFLGFAQVWCSVRTPESSHEGLITDPHSPSRFRVIGSLS 744

Qy    723 NSEEFQKAFNCPPNSTMNRGMDSCRLW 749
          ||:|| : | ||| | ||     | :|
Db    745 NSKEFSEHFRCPPGSPMN-PPHKCEVW 770
```

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RESULT 9
ECE1_RAT
ID   ECE1_RAT       STANDARD;      PRT;   762 AA.
AC   P42893; Q9WUY8; Q9WUY9;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Endothelin-converting enzyme 1 (EC 3.4.24.71) (ECE-1).
GN   ECE1.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM C).
RC   TISSUE=Endothelial cells;
RX   MEDLINE=94308046; PubMed=8034569;
RA   Shimada K., Takahashi M., Tanzawa K.;
RT   "Cloning and functional expression of endothelin-converting enzyme
RT   from rat endothelial cells.";
RL   J. Biol. Chem. 269:18275-18278(1994).
RN   [2]
RP   SEQUENCE OF 1-116 FROM N.A., ALTERNATIVE SPLICING, SUBCELLULAR
RP   LOCATION, AND TISSUE SPECIFICITY.
RC   TISSUE=Smooth muscle;
RX   MEDLINE=99421637; PubMed=10491078;
RA   Valdenaire O., Lepailleur-Enouf D., Egidy G., Thouard A., Barret A.,
RA   Vranckx R., Tougard C., Michel J.-B.;
RT   "A fourth isoform of endothelin-converting enzyme (ECE-1) is generated
RT   from an additional promoter.";
RL   Eur. J. Biochem. 264:341-349(1999).
RN   [3]
RP   SEQUENCE OF 1-109 FROM N.A. (ISOFORM A).
RC   STRAIN=Sprague-Dawley; TISSUE=Lung;
RX   MEDLINE=95402196; PubMed=7672114;
RA   Shimada K., Takahashi M., Ikeda M., Tanzawa K.;
RT   "Identification and characterization of two isoforms of an
RT   endothelin-converting enzyme-1.";
RL   FEBS Lett. 371:140-144(1995).
CC   -!- FUNCTION: CONVERTS BIG ENDOTHELIN-1 TO ENDOTHELIN-1.
CC   -!- CATALYTIC ACTIVITY: Forms endothelin 1 by cleavage of the 21-
CC       Trp-|-Val-22 bond in the precursor.
CC   -!- ENZYME REGULATION: INHIBITED BY PHOSPHORAMIDON (BY SIMILARITY).
CC   -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein.
CC   -!- ALTERNATIVE PRODUCTS: 4 ISOFORMS; A (SHOWN HERE), B, C AND D; ARE
CC       PRODUCED BY ALTERNATIVE SPLICING.
CC   -!- TISSUE SPECIFICITY: ALL ISOFORMS ARE EXPRESSED IN AORTIC
CC       ENDOTHELIAL CELLS. ISOFORM A IS ALSO EXPRESSED IN LIVER; ISOFORM B
CC       IN SMOOTH MUSCLE CELLS AND FIBROBLASTS; ISOFORM C IN AORTIC
CC       ENDOTHELIAL CELLS, SMOOTH MUSCLE CELLS, FIBROBLASTS, LIVER AND
CC       LUNG, AND ISOFORM D IN SMOOTH MUSCLE CELLS.
CC   -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M13.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; D29683; BAA06152.1; -.
DR   EMBL; AJ130826; CAB46528.1; -.
DR   EMBL; AJ130827; CAB46529.1; -.
DR   EMBL; D63795; BAA09864.1; -.
DR   HSSP; P08473; 1DMT.
DR   MEROPS; M13.002; -.
DR   InterPro; IPR000718; Peptidase_M13.
DR   InterPro; IPR000130; Zn_MTpeptdse.
DR   Pfam; PF01431; Peptidase_M13; 1.
DR   PRINTS; PR00786; NEPRILYSIN.
DR   PROSITE; PS00142; ZINC_PROTEASE; 1.
KW   Hydrolase; Metalloprotease; Zinc; Glycoprotein; Transmembrane;
KW   Signal-anchor; Alternative splicing.
FT   DOMAIN        1     60       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     61     81       SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT                                (POTENTIAL).
FT   DOMAIN       82    762       EXTRACELLULAR (POTENTIAL).
FT   METAL       599    599       ZINC (CATALYTIC) (BY SIMILARITY).
FT   ACT_SITE    600    600       BY SIMILARITY.
FT   METAL       603    603       ZINC (CATALYTIC) (BY SIMILARITY).
FT   METAL       659    659       ZINC (CATALYTIC) (BY SIMILARITY).
FT   ACT_SITE    663    663       PROTON DONOR (BY SIMILARITY).
FT   CARBOHYD    158    158       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    179    179       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    202    202       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    262    262       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    308    308       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    354    354       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    375    375       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    531    531       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    624    624       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    643    643       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC      1     36       MGSLRPPQGLGLQWSSFFLGKKGPGLTVSLPLLASS -> M
FT                                RTVWPPLRAALAALGMSSYKRATLDEEDLVDSLSEGDVYPN
FT                                G (IN ISOFORM B).
FT   VARSPLIC      1     36       MGSLRPPQGLGLQWSSFFLGKKGPGLTVSLPLLASS -> M
FT                                MSSYKRATLDEEDLVDSLSEGDVYPNG (IN ISOFORM
FT                                C).
FT   VARSPLIC      1     36       MGSLRPPQGLGLQWSSFFLGKKGPGLTVSLPLLASS -> M
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FT                                   ETLRESVLHLALQMSSYKRATLDEEDLVDSLSEGDVYPNG
FT                                   (IN ISOFORM D).
SQ   SEQUENCE   762 AA;  86125 MW;  D6B8253BC67CCAD8 CRC64;

  Query Match             31.4%;  Score 1243.5;  DB 1;  Length 762;
  Best Local Similarity   37.5%;  Pred. No. 4.6e-76;
  Matches  277;  Conservative  129;  Mismatches  284;  Indels   49;  Gaps   19;

Qy      23 LVVFVGGTLVLGTILFLVSQGLLSLQAKQEYCLKPECIEAAAAILSKVNLSVDPCDNFFR 82
           ||| |   |  | :  | : |:          ||   |:   ::||: :: :|||| :||
Db      61 LVVLV-TLLAAGLVACLAALGIQYRTRTPPVCLTEACVSVTSSILNSMDPTVDPCQDFFS 119

Qy      83 FACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLEKSISRRRDTEAIQKAKILYSSC 142
           :|| |||  ||:|:    :| :  |  :    :| ||| | :    :|| :||:: | :|
Db     120 YACGGWIKANPVPDGHSRWGTFSNLWEHNQAIIKHLLENSTASA--SEAEKKAQVYYRAC 177

Qy     143 MNEKAIEKADAKPLLHILRHSPFRWPVLESNIGPEGVWSERKFSLLQTLATFRGQYSNSV 202
           |||  ||:  ||||: ::      | :       | |::  |    ||      |  |
Db     178 MNETRIEELRAKPLMELIEKLG-GWNI-------TGPWAKDNFQ--DTLQVVTAHYRTSP 227

Qy     203 FIRLYVSPDDKASNEHILKLDQATLSLAVREDYLDNSTEAKSYRDALYKFMVDTAVLL-G 261
           |  :||| | | || :::::||: | |  |: || | || :        :||    || |
Db     228 FFSVYVSADSKNSNSNVIQVDQSGLGLPSRDYYL-NKTENEKVLTGYLNYMVQLGKLLGG 286

Qy     262 ANSSRAEHDMKSVLRLEIKIAEIMIPHENRTSEAM-YNKMNISELSAMIPQFDWLGYIKK 320
           :       |: :|  |  :| | || | |  | : |:|:  :||  : |  :|| ::
Db     287 GDEDSIRPQMQQILDFETALANITIPQEKRRDEELIYHKVTAAELQTLAPAINWLPFLNA 346

Qy     321 VIDTRLYPHLKDISPSENVVVRVPQYFKDLFRILGSERKKTIANYLVWRMVYSRIPNLSR 380
           :     ||   :|: || :||   :| : :  :: |  |  : ||::| :|      | :
Db     347 I----FYP--VEINESEPIVVYDKEYLRQVSTLINSTDKCLLNNYMMWNLVRKTSSFLDQ 400

Qy     381 RFQYRWLEFSRVIQGT-TTLLPQWDKCVNFIESALPYVVGKMFVDVYFQEDKKEMMEELV 439
           |||    :|  |: ||  | ||:|  ||:  |: | : :| |||   | || | :  |::
Db     401 RFQDADEKFMEVMYGTKKTCLPRWKFCVSDTENNLGFALGPMFVKATFAEDSKNIASEII 460

Qy     440 EGVRWAFIDMLEKENEWMDAGTKRKAKEKARAVLAKVGYPEFIM---------NDTHVNE 490
             :: || : |    :|||  |:| ||||| |:   :||| |||          ||
Db     461 LEIKKAFEESL-STLKWMDEDTRRSAKEKADAIYNMIGYPNFIMDPKELDKVFNDYTAVP 519

Qy     491 DLKAIKFSEADYFGNVLQTRKYLAQSDFFWLRKAVPKTEWFTNPTTVNAFYSASTNQIRF 550
           ||          || | ::   :  :      ||||  : :|   |  |||:|| : |:| |
Db     520 DL---------YFENAMRFFNFSLRVTADQLRKAPNRDQWSMTPPMVNAYYSPTKNEIVF 570

Qy     551 PAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNGRKYDKNGNLDPWWSTESEEK 610
           ||| || ||:  :  | :|::| |||:|||| || ||: ||:|||:||| |||   | |
Db     571 PAGILQAPFYTRSS-PNALNFGGIGVVVGHELTHAFDDQGREYDKDGNLRPWWKNSSVEA 629

Qy     611 FKEKTKCMINQYSNYYWKKAGLNVKGKRTLGENIADNGGLREAFRAYRKWINDRRQGLEE 670
           ||::|:||: ||:||      |  | |: ||||||||||||: |:|||: |:  :: | |:
Db     630 FKQQTECMVQQYNNY--SVNGEPVNGRHTLGENIADNGGLKAAYRAYQNWV--KKNGAEQ 685

Qy     671 PLLPGITFTNNQLFFLSYAHVRCNSYRPEAAREQVQIGAHSPPQFRVNGAISNSEEFQKA 730
           :|| :  |:|||||| :| | |:   ||:: | :    ||| :||| |::|||:|| :
Db     686 -ILPTLGLTSNQLFFLGFAQVWCSVRTPESSHEGLITDPHSPSRFRVIGSLSNSKEFSEH 744

Qy     731 FNCPPNSTMNRGMDSCRLW 749
           | ||  | ||     | :|
Db     745 FRCPLGSPMN-PRHKCEVW 762


RESULT 10
ECE1_BOVIN
ID   ECE1_BOVIN     STANDARD;      PRT;   754 AA.
AC   P42891;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Endothelin-converting enzyme 1 (EC 3.4.24.71) (ECE-1).
GN   ECE1.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX   MEDLINE=95104423; PubMed=7805846;
RA   Schmidt M., Kroeger B., Jacob E., Seulberger H., Subkowski T.,
RA   Otter R., Meyer T., Schmalzing G., Hillen H.;
RT   "Molecular characterization of human and bovine endothelin converting
RT   enzyme (ECE-1).";
RL   FEBS Lett. 356:238-243(1994).
CC   -!- FUNCTION: CONVERTS BIG ENDOTHELIN-1 TO ENDOTHELIN-1.
CC   -!- CATALYTIC ACTIVITY: Forms endothelin 1 by cleavage of the 21-
CC       Trp-|-Val-22 bond in the precursor.
CC   -!- ENZYME REGULATION: INHIBITED BY PHOSPHORAMIDON.
CC   -!- SUBUNIT: HOMODIMER.
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein.
CC   -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M13.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Z35306; CAA84547.1; -.
DR   HSSP; P08473; 1DMT.
DR   MEROPS; M13.002; -.
DR   InterPro; IPR000718; Peptidase_M13.
DR   InterPro; IPR000130; Zn_MTpeptdse.
DR   Pfam; PF01431; Peptidase_M13; 1.
DR   PRINTS; PR00786; NEPRILYSIN.
DR   PROSITE; PS00142; ZINC_PROTEASE; 1.
KW   Hydrolase; Metalloprotease; Zinc; Glycoprotein; Transmembrane;
KW   Signal-anchor.
FT   DOMAIN        1      52       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     53      73       SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT                                 (POTENTIAL).
FT   DOMAIN       74     754       EXTRACELLULAR (POTENTIAL).
FT   METAL       591     591       ZINC (CATALYTIC) (BY SIMILARITY).
FT   ACT_SITE    592     592       BY SIMILARITY.
FT   METAL       595     595       ZINC (CATALYTIC) (BY SIMILARITY).
FT   METAL       651     651       ZINC (CATALYTIC) (BY SIMILARITY).
FT   ACT_SITE    655     655       PROTON DONOR (BY SIMILARITY).
FT   CARBOHYD    150     150       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    171     171       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    194     194       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    254     254       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    300     300       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    346     346       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    367     367       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    523     523       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    616     616       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    635     635       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   754 AA;  85616 MW;  E9276CCCB8E6FF4C CRC64;

  Query Match             31.4%;  Score 1241.5;  DB 1;  Length 754;
  Best Local Similarity   37.9%;  Pred. No. 6.2e-76;
  Matches  282;  Conservative  120;  Mismatches  282;  Indels   61;  Gaps   21;

Qy      23 LVVFVGGTLVLGTILFLVSQGLLSLQAKQEYCLKPECIEAAAAILSKVNLSVDPCDNFFR 82
           ||| |   |    :  |   |:          ||   ||   ::||| :: :|||| :||
Db      53 LVVLV-ALLAAALVACLAVLGIQYQTRTPSVCLSEACISVTSSILSSMDPTVDPCQDFFT 111

Qy      83 FACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLEKSISRRRDTEAIQKAKILYSSC 142
           :|| |||  ||:|:    :| :  |  :    :| ||| | :    :|| :| :  | :|
Db     112 YACGGWIKANPVPDGHSRWGTFSNLWEHNQAIIKHLLENSTA--SVSEAERKDQEYYRAC 169

Qy     143 MNEKAIEKADAKPLLHILRHSPFRWPVLESNIGPEGVWSERKFSLLQTLATFRGQYSNSV 202
           |||  ||:  ||||: ::      | :       | | :  |    ||      |  |
Db     170 MNETRIEELKAKPLMELIEKLG-GWNI-------TGPWDKDNFQ--DTLQVVTSHYHTSP 219
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Qy     203 FIRLYVSPDDKASNEHILKLDQATLSLAVREDYLDNSTEAKSYRDALYKFMVDTAVLLGA 262
           |  :||| | | || :::::||: | |   |: || | || :         :||    |||
Db     220 FFSVYVSADSKNSNSNVIQVDQSGLGLPSRDYYL-NKTENEKVLTGYLNYMVQLGKLLGG 278

Qy     263 NS-SRAEHDMKSVLRLEIKIAEIMIPHENRTSEAM-YNKMNISELSAMIPQFDWLGYIKK 320
           :       |: :|  |  :| | || | |  | : |:|:  :||  :  |  :|| :
Db     279 GAEDTIRPQMQQILDFETALANITIPQEKRRDEELIYHKVTAAELQTLAPAINWLPF--- 335

Qy     321 VIDTRLYPHLKDISPSENVVVRVPQYFKDLFRILGSERKKTIANYLVWRMVYSRIPNLSR 380
           ::|  ||   :|: || :|:   :|   :  :: |  |  : ||::| :|      | :
Db     336 -LNTIFYP--VEINESEPIVIYDKEYLSKVSTLINSTDKCLLNNYMIWNLVRKTSSFLDQ 392

Qy     381 RFQYRWLEFSRVIQGT-TTLLPQWDKCVNFIESALPYVVGKMFVDVYFQEDKKEMMEELV 439
           |||    :|  |: ||  | ||:|  ||:  |: | : :| |||   | || | :  |::
Db     393 RFQDADEKFMEVMYGTKKTCLPRWKFCVSDTENTLGFALGPMFVKATFAEDSKNIASEII 452

Qy     440 EGVRWAFIDMLEKENEWMDAGTKRKAKEKARAVLAKVGYPEFIM---------NDTHVNE 490
             :: || : |    :|||  |:: ||||| |:   :||| |||          ||
Db     453 LEIKKAFEESL-STLKWMDEDTRKSAKEKADAIYNMIGYPNFIMDPKELDKVFNDYTAVP 511

Qy     491 DLKAIKFSEADYFGNVLQTRKYLAQSDFFW------LRKAVPKTEWFTNPTTVNAFYSAS 544
           ||         || | ::        :| |       ||||  : :|   |  |||:|| :
Db     512 DL---------YFENAMRF------FNFSWRVTADQLRKAPNRDQWSMTPPMVNAYYSPT 556

Qy     545 TNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNGRKYDKNGNLDPWWS 604
             |:| |||| || ||:  :  | :|::| |||:|||| || ||: ||:|||:||| |||
Db     557 KNEIVFPAGILQAPFYTRSS-PNALNFGGIGVVVGHELTHAFDDQGREYDKDGNLRPWWK 615

Qy     605 TESEEKFKEKTKCMINQYSNYYWKKAGLNVKGKRTLGENIADNGGLREAFRAYRKWINDR 664
             | | ||::| ||: || ||      |  | |: ||||||||||||: |:|||: |:  :
Db     616 NSSVEAFKQQTACMVEQYGNY--SVNGEPVNGRHTLGENIADNGGLKAAYRAYQNWV--K 671

Qy     665 RQGLEEPLLPGITFTNNQLFFLSYAHVRCNSYRPEAAREQVQIGAHSPPQFRVNGAISNS 724
           : | |:  || :  ||||||||:| | |:   ||:: | :    ||| :||| |:|||| 
Db     672 KNGAEQ-TLPTLGLTNNQLFFLSFAQVWCSVRTPESSHEGLITDPHSPSRFRVIGSISNS 730

Qy     725 EEFQKAFNCPPNSTMNRGMDSCRLW 749
           :|| : |:||| | ||     | :|
Db     731 KEFSEHFHCPPGSPMN-PHHKCEVW 754
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RESULT 11
ECE2_HUMAN
ID ECE2_HUMAN STANDARD; PRT; 787 AA.
AC O60344; Q96NX4; Q96NX3;
DT 30-MAY-2000 (Rel. 39, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Endothelin-converting enzyme 2 (EC 3.4.24.71) (ECE-2).
GN ECE2 OR KIAA0604.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS A; B AND C).
RA Lorenzo M.-N., Khan R.Y., Wang Y., Tai S.C., Chan G.C., Cheung A.H.,
RA Marsden P.A.;
RT "Human endothelin converting enzyme-2 (ECE2): characterization of mRNA
RT species and chromosomal localization.";
RL Biochim. Biophys. Acta 0:0-0(2002).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM B).
RC TISSUE=Brain;
RX MEDLINE=98290545; PubMed=9628581;
RA Nagase T., Ishikawa K.-I., Miyajima N., Tanaka A., Kotani H.,
RA Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. IX.
RT The complete sequences of 100 new cDNA clones from brain which can
RT code for large proteins in vitro.";
RL DNA Res. 5:31-39(1998).
CC -!- FUNCTION: CONVERTS BIG ENDOTHELIN-1 TO ENDOTHELIN-1 (BY
CC SIMILARITY).
CC -!- CATALYTIC ACTIVITY: Forms endothelin 1 by cleavage of the 21-
CC Trp-|-Val-22 bond in the precursor.
CC -!- SUBCELLULAR LOCATION: Type II membrane protein.
CC -!- ALTERNATIVE PRODUCTS: 3 isoforms; ECE-2A (shown here), ECE-2B and
CC ECE-2C; are produced by alternative splicing.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M13.
CC ---

CC ---
DR EMBL; AF428263; AAL30386.1; -.
DR EMBL; AF428264; AAL30387.1; -.
DR EMBL; AF192531; AAG28399.1; -.
DR EMBL; AB011176; BAA25530.1; -.
DR HSSP; P08473; 1DMT.
DR MEROPS; M13.003; -.
DR InterPro; IPR000718; Peptidase_M13.
DR InterPro; IPR000130; Zn_MTpeptdse.
DR Pfam; PF01431; Peptidase_M13; 1.
DR PRINTS; PR00786; NEPRILYSIN.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
KW Hydrolase; Metalloprotease; Zinc; Glycoprotein; Transmembrane;
KW Signal-anchor; Alternative splicing.

FT	DOMAIN	1	82	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	83	103	SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).
FT	DOMAIN	104	787	EXTRACELLULAR (POTENTIAL).
FT	METAL	624	624	ZINC (CATALYTIC) (BY SIMILARITY).
FT	ACT_SITE	625	625	BY SIMILARITY.
FT	METAL	628	628	ZINC (CATALYTIC) (BY SIMILARITY).
FT	METAL	684	684	ZINC (CATALYTIC) (BY SIMILARITY).
FT	ACT_SITE	688	688	PROTON DONOR (BY SIMILARITY).
FT	CARBOHYD	183	183	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	187	187	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	228	228	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	288	288	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	333	333	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	400	400	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	556	556	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	649	649	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	657	657	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARSPLIC	1	63	MQARHAHVPQLRWETMDVRKLDFPSASFDVVLEKGTLDALL AGERDPWTVSSEGVHTVDQVLS -> MNVALQELGAGSNMV EYKRATLRDEDAPETPVEGGASPDAM (IN ISOFORM ECE-2B).
FT	VARSPLIC	1	64	MQARHAHVPQLRWETMDVRKLDFPSASFDVVLEKGTLDALL AGERDPWTVSSEGVHTVDQVLSE -> MNVALQELGAGSN (IN ISOFORM ECE-2C).

SQ SEQUENCE 787 AA; 89221 MW; CC2D2B0F0EBF7239 CRC64;

Query Match 30.8%; Score 1221; DB 1; Length 787;
Best Local Similarity 35.2%; Pred. No. 1.6e-74;
Matches 264; Conservative 144; Mismatches 303; Indels 38; Gaps 17;

```
Qy      10 ETGKKANRGTRIAL-VVFVGGTLVLGTILF--LVSQGL-LSLQAKQEYCLKPECIEAAAA 65
           : | :   |:|  | :|  | :|:|  :|   ||: |:           ||   ||  |
Db      68 QKGTRQLLGSRTQLELVLAGASLLLAALLLGCLVALGVQYHRDPSHSTCLTEACIRVAGK 127

Qy      66 ILSKVNLSVDPCDNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLEKSISR 125
           ||  ::  | ||::|::|:| |||  ||:|:    :  :. |        || ||| : :
Db     128 ILESLDRGVSPCEDFYQFSCGGWIRRNPLPDGRSRWNTFNSLWDQNQAILKHLLENT-TF 186

Qy     126 RRDTEAIQKAKILYSSCMNEKAIEKADAKPLLHILRHSPFRWPVLESNIGP---EGVWSE 182
             :|| || :  | ||:  : ||:  |:||  ::            ||     | | :
Db     187 NSSSEAEQKTQRFYLSCLQVERIEELGAQPLRDLI----------EKIGGWNITGPWDQ 235

Qy     183 RKFSLLQTLATFRGQYSNSVFIRLYVSPDDKASNEHILKLDQATLSLAVREDYLDNSTEA 242
             | :: |    | |  : |  :|:| | |:|| :::::||: | |  |: || | |
```

```
Db    236 DNF--MEVLKAVAGTYRATPFFTVYISADSKSSNSNVIQVDQSGLFLPSRDYYL-NRTAN 292

Qy    243 KSYRDALYKFMVDTAVLLGANSSRAEHDMKSVLRLEIKIAEIMIPH-ENRTSEAMYNKMN 301

Db    293 EKVLTAYLDYMEELGMLLGGRPTSTREQMQQVLELEIQLANITVPQDQRRDEEKIYHKMS 352

Qy    302 ISELSAMIPQFDWLGYIKKVIDTRLYPHLKDISPSENVVVRVPQYFKDLFRILGSERKKT 361

Db    353 ISELQALAPSMDWLEFLSFLLSP------LELSDSEPVVVYGMDYLQQVSELINRTEPSI 406

Qy    362 IANYLVWRMVYSRIPNLSRRFQYRWLEFSRVIQGT-TTLLPQWDKCVNFIESALPYVVGK 420

Db    407 LNNYLIWNLVQKTTSSLDRRFESAQEKLLETLYGTKKSCVPRWQTCISNTDDALGFALGS 466

Qy    421 MFVDVYFQEDKKEMMEELVEGVRWAFIDMLEKENEWMDAGTKRKAKEKARAVLAKVGYPE 480

Db    467 LFVKATFDRQSKEIAEGMISEIRTAFEEAL-GQLVWMDEKTRQAAKEKADAIYDMIGFPD 525

Qy    481 FIMNDTHVNEDLKAIKFSEADYFGNVLQTRKYLAQSDFFWLRKAVPKTEWFTNPTTVNAF 540

Db    526 FILEPKELDDVYDGYEISEDSFFQNMLNLYNFSAKVMADQLRKPPSRDQWSMTPQTVNAY 585

Qy    541 YSASTNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNGRKYDKNGNLD 600

Db    586 YLPTKNEIVFPAGILQAPFY-ARNHPKALNFGGIGVVMGHELTHAFDDQGREYDKEGNLR 644

Qy    601 PWWSTESEEKFKEKTKCMINQYSNYYWKKAGLNVKGKRTLGENIADNGGLREAFRAYRKW 660

Db    645 PWWQNESLAAFRNHTACMEEQYNQY--QVNGERLNGRQTLGENIADNGGLKAAYNAYKAW 702

Qy    661 INDRRQGLEEPLLPGITFTNNQLFFLSYAHVRCNSYRPEAAREQVQIGAHSPPQFRVNGA 720

Db    703 L--RKHG-EEQQLPAVGLTNHQLFFVGFAQVWCSVRTPESSHEGLVTDPHSPARFRVLGT 759

Qy    721 ISNSEEFQKAFNCPPNSTMNRGMDSCRLW 749

Db    760 LSNSRDFLRHFGCPVGSPMNPG-QLCEVW 787


RESULT 12
ECE2_BOVIN
ID   ECE2_BOVIN     STANDARD;      PRT;   787 AA.
AC   Q10711;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Endothelin-converting enzyme 2 (EC 3.4.24.71) (ECE-2).
GN   ECE2.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95318093; PubMed=7797512;
RA   Emoto N., Yanagisawa M.;
RT   "Endothelin-converting enzyme-2 is a membrane-bound, phosphoramidon-
RT   sensitive metalloprotease with acidic pH optimum.";
RL   J. Biol. Chem. 270:15262-15268(1995).
CC   -!- FUNCTION: CONVERTS BIG ENDOTHELIN-1 TO ENDOTHELIN-1. OPTIMUM PH IS
CC       5.5. INACTIVE AT NEUTRAL PH.
CC   -!- CATALYTIC ACTIVITY: Forms endothelin 1 by cleavage of the 21-
CC       Trp-|-Val-22 bond in the precursor.
CC   -!- ENZYME REGULATION: INHIBITED BY PHOSPHORAMIDON.
CC   -!- SUBUNIT: HOMODIMER.
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein.
CC   -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M13.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U27341; AAA82927.1; -.
DR   HSSP; P08473; 1DMT.
DR   MEROPS; M13.003; -.
DR   InterPro; IPR000718; Peptidase_M13.
DR   InterPro; IPR000130; Zn_MTpeptdse.
DR   Pfam; PF01431; Peptidase_M13; 1.
DR   PRINTS; PR00786; NEPRILYSIN.
DR   PROSITE; PS00142; ZINC_PROTEASE; 1.
KW   Hydrolase; Metalloprotease; Zinc; Glycoprotein; Transmembrane;
KW   Signal-anchor.
FT   DOMAIN          1     82       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM       83    103       SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT                                  (POTENTIAL).
FT   DOMAIN        104    787       EXTRACELLULAR (POTENTIAL).
FT   METAL         624    624       ZINC (CATALYTIC) (BY SIMILARITY).
FT   ACT_SITE      625    625       BY SIMILARITY.
FT   METAL         628    628       ZINC (CATALYTIC) (BY SIMILARITY).
FT   METAL         684    684       ZINC (CATALYTIC) (BY SIMILARITY).
FT   ACT_SITE      688    688       PROTON DONOR (BY SIMILARITY).
FT   CARBOHYD      164    164       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD      183    183       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD      187    187       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD      228    228       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD      288    288       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD      333    333       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD      400    400       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD      556    556       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD      649    649       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD      657    657       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   787 AA;  88957 MW;  F085C2921DAF0BF2 CRC64;

  Query Match             29.9%;  Score 1184;  DB 1;  Length 787;
  Best Local Similarity   35.1%;  Pred. No. 4.9e-72;
  Matches  265;  Conservative  138;  Mismatches  313;  Indels   38;  Gaps   18;

Qy      4 ETGSSVETGKKANRGTRIALVVFVGGTLVLGTILF--LVSQGL-LSLQAKQEYCLKPECI 60

Db     64 EAGFRKRTSRLLGLHTQLELVL-AGVSLLLAALLLGCLVALGVQYHRDPSHSTCLTEACI 122

Qy     61 EAAAAILSKVNLSVDPCDNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLE 120

Db    123 RVAGKILESLDRGVSPCEDFYQFSCGGWIRRNPLPDGRSRWNNSNSLWDQNQAILKHLLE 182

Qy    121 KSISRRRDTEAIQKAKILYSSCMNEKAIEKADAKPLLHILRHSPFRWPVLESNIG---PE 177

Db    183 NT-TFNSSSEAERKTQRFYLSCLQVERIEELGA----HALRD-------LIDKIGGWNVT 230

Qy    178 GVWSERKFSLLQTLATFRGQYSNSVFIRLYVSPDDKASNEHILKLDQATLSLAVREDYLD 237

Db    231 GPWDQDNF--MEVLKAVAGTYRATPFFTVYVSADSKSSNSNIIQVDQSGLFLPSRDYYL- 287

Qy    238 NSTEAKSYRDALYKFMVDTAVLLGANSSRAEHDMKSVLRLEIKIAEIMIPH-ENRTSEAM 296

Db    288 NRTANEKVLTAYLDYMEELGMLLGGQPTSTREQMRQVLELEIQLANITVPQDQRRDEEKI 347

Qy    297 YNKMNISELSAMIPQFDWLGYIKKVIDTRLYPHLKDISPSENVVVRVPQYFKDLFRILGS 356

Db    348 YHKMSIAELQALAPSMDWLEFLSFLLSP------LELGDSEPVVVYGTDYLQQVSELINR 401

Qy    357 ERKKTIANYLVWRMVYSRIPNLSRRFQYRWLEFSRVIQGT-TTLLPQWDKCVNFIESALP 415

Db    402 TEPSVLNNYLIWNLVQKTTSSLDHRFESAQEKLLETLYGTKKSCTPRWQTCISNTDDALG 461

Qy    416 YVVGKMFVDVYFQEDKKEMMEELVEGVRWAFIDMLEKENEWMDAGTKRKAKEKARAVLAK 475

Db    462 FALGSLFVKATFDRQSKEIAEGMISEIRVAFEEAL-GHLVWMDEKTRQAAKEKADAIYDM 520

Qy    476 VGYPEFIMNDTHVNEDLKAIKFSEADYFGNVLQTRKYLAQSDFFWLRKAVPKTEWFTNPT 535
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Db    521 IGFPDFILEPKELDDVYDGYEVSEDSFFQNMLNLYNFSAKVMADQLRKPPSRDQWSMTPQ 580

Qy    536 TVNAFYSASTNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNGRKYDK 595

Db    581 TVNAYYLPTKNEIVFPAGILQAPFY-TCNHPQALNFGGIGVVMGHELTHAFDDQGREYDK 639

Qy    596 NGNLDPWWSTESEEKFKEKTKCMINQYSNYYWKKAGLNVKGKRTLGENIADNGGLREAFR 655

Db    640 EGNLRPWWQNESLAAFRNHTACIEEQYSQY--QVNGEKLNGRQTLGENIADNGGLKAAYN 697

Qy    656 AYRKWINDRRQGLEEPLLPGITFTNNQLFFLSYAHVRCNSYRPEAAREQVQIGAHSPPQF 715

Db    698 AYKAWL--RKHG-EEQQLPAVGLTNHQLFFVGFAQVWCSVRTPESSHEGLVTDPHSPARF 754

Qy    716 RVNGAISNSEEFQKAFNCPPNSTMNRGMDSCRLW 749

Db    755 RVLGTLSNSRDFLRHFGCPVGSPMNSG-QLCEVW 787
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RESULT 13
ECEL_MOUSE
ID   ECEL_MOUSE   STANDARD;   PRT;   775 AA.
AC   Q9JMI0;
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Endothelin-converting enzyme-like 1 (EC 3.4.24.-) (Xce protein)
DE   (Damage-induced neuronal endopeptidase).
GN   ECEL1 OR XCE OR DINE.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=20226106; PubMed=10759559;
RA   Kiryu-Seo S., Sasaki M., Yokohama H., Nakagomi S., Hirayama T.,
RA   Aoki S., Wada K., Kiyama H.;
RT   "Damage-induced neuronal endopeptidase (DINE) is a unique
RT   metallopeptidase expressed in response to neuronal damage and
RT   activates superoxide scavengers.";
RL   Proc. Natl. Acad. Sci. U.S.A. 97:4345-4350(2000).
CC   -!- FUNCTION: May contribute to the degradation of peptide hormones
CC   and be involved in the inactivation of neuronal peptides.
CC   -!- COFACTOR: Binds 1 zinc ion (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein (By similarity).
CC   -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M13.
CC   ---
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CC   or send an email to license@isb-sib.ch).
CC   ---
DR   EMBL; AB026294; BAA95005.1; -.
DR   HSSP; P08473; 1DMT.
DR   MEROPS; M13.007; -.
DR   MGD; MGI:1343461; Ece1.
DR   InterPro; IPR000718; Peptidase_M13.
DR   InterPro; IPR000130; Zn_MTpeptdse.
DR   Pfam; PF01431; Peptidase_M13; 1.
DR   PRINTS; PR00786; NEPRILYSIN.
DR   PROSITE; PS00142; ZINC_PROTEASE; 1.
KW   Hydrolase; Protease; Metalloprotease; Metal-binding; Zinc;
KW   Glycoprotein; Transmembrane; Signal-anchor.
FT   DOMAIN   1   61   CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM   62   82   SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT   (POTENTIAL).
FT   DOMAIN   83   775   LUMENAL (POTENTIAL).
FT   METAL   612   612   ZINC (CATALYTIC) (BY SIMILARITY).
FT   ACT_SITE   613   613   BY SIMILARITY.
FT   METAL   616   616   ZINC (CATALYTIC) (BY SIMILARITY).
FT   METAL   672   672   ZINC (CATALYTIC) (BY SIMILARITY).
FT   CARBOHYD   255   255   N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   322   322   N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   656   656   N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   775 AA; 87993 MW; 53A4595D7C5F34B9 CRC64;

 Query Match   25.1%; Score 992; DB 1; Length 775;
 Best Local Similarity 30.7%; Pred. No. 3.9e-59;
 Matches 241; Conservative 159; Mismatches 290; Indels   94; Gaps   22;

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Qy     11 TGKKANRGTRIAL-------VVFVGGTLVLGTILFLVSQGLLSLQ----------AKQE 52

Db     41 SGRSAS-GSRSGLPRWNRREVCLLSG-LVFAAGLCAILAAMLALKYLGPGAAGGGGACPE 98

Qy     53 YCLKPECIEAAAAILS-KVNLSVDPCDNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNV 111

Db     99 GCPERKAFARAARFLSANLDASIDPCQDFYSFACGGWLRRHAIPDDKLTYGTIAAIGEQN 158

Qy    112 DLKLKELLEKSISRRRDT-----EAIQKAKILYSSCMNEKAIEKADAKPLLHILRHSPFR 166

Db    159 EERLRRLL------ARPTGGPGGAAQRKVRAFFRSCLDMREIERLGPRPMLEVIEDC--- 209

Qy    167 WPVLESNIGPEGVW---------SERKFSLLQTLATFRGQYSNSVFIRLYVSPDDKASNE 217

Db    210 ----------GGWDLGGAADRPGAARWDLNRLLYKAQGVYSAAALFSLTVSLDDRNSSR 258

Qy    218 HILKLDQATLSLAVREDYLDNSTEAKSYRDALYKFMVDTAVLLGANSSRAEHDMKSVLRL 277

Db    259 YVIRIDQDGLTLPERTLYLAQDEESEKILAAYRVFMQRLLRLLGADA--VEQKAQEILQL 316

Qy    278 EIKIAEIMIPHEN---RTSEAMYNKMNISELSAMIPQFDWLGYIKKVIDTRLYPHLKDIS 334

Db    317 EQRLANISVSEYDDLRRDVSSAYNKVTLGQLQKIIPHLQWKWLLDQIFQ-------EDFS 369

Qy    335 PSENVVVRVPQYFKDLFRILGSERKKTIANYLVWRMVYSRIPNLSRRFQYRWLEFSRVIQ 394

Db    370 EEEEVVLLATDYMQQVSQLIRSTPRRILHNYLVWRVVVVLSEHLSSPFREALHELAKEME 429

Qy    395 GTTTLLPQWDK-------CVNFIESALPYVVGKMFVDVYFQEDKKEMMEELVEGVRWAFI 447

Db    430 GN-------DKPQELARVCLGQANRHFGMALGALFVHEHFSAASKAKVQQLVEDIKYILG 482

Qy    448 DMLEKENEWMDAGTKRKAKEKARAVLAKVGYPEFIMNDTHVNEDLKAIKFSEADYFGNVL 507

Db    483 QRLE-ELDWMDAQTKAAARAKLQYMMVMVGYPDFLLKPEAVDKEYE-FEVHEKTYFKNIL 540

Qy    508 QTRKYLAQSDFFWLRKAVPKTEWFTNPTTVNAFYSASTNQIRFPAGELQKPFFWGTEYPR 567

Db    541 NSIRFSIQLSVKKIRQEVDKSTWLLPPQALNAYYLPNKNQMVYPAGILQ-PTLYDPDFPQ 599

Qy    568 SLSYGAIGVIVGHEFTHGFDNNGRKYDKNGNLDPWWSTESEEKFKEKTKCMINQYSNY-- 625

Db    600 SLNYGGIGTIIGHELTHGYDDWGGQYDRSGNLLHWWTEASYSRFLHKAECIVRLYDNFTV 659

Qy    626 YWKKAGLNVKGKRTLGENIADNGGLREAFRAYRKWINDRRQGLEEPLLPGITFTNNQLFF 685

Db    660 YNQR----VNGKHTLGENIADMGGLKLAYYAYQKWV--REHGPEHP-LHRLKYTHNQLFF 712

Qy    686 LSYAHVRCNSYRPEAAREQVQIGAHSPPQFRVNGAISNSEEFQKAFNCPPNSTMNRGMDS 745

Db    713 IAFAQNWCIKRRSQSIYLQVLTDKHAPEHYRVLGSVSQFEEFGRAFHCPKDSPMN-PVHK 771

Qy    746 CRLW 749

Db    772 CSVW 775
```

RESULT 14
ECEL_RAT
ID   ECEL_RAT   STANDARD;   PRT;   775 AA.
AC   Q9JHL3; Q9Z192;

```
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Endothelin-converting enzyme-like 1 (EC 3.4.24.-) (Xce protein)
DE   (Damage-induced neuronal endopeptidase).
GN   ECEL1 OR XCE OR DINE.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Wistar; TISSUE=Brain;
RX   MEDLINE=20226106; PubMed=10759559;
RA   Kiryu-Seo S., Sasaki M., Yokohama H., Nakagomi S., Hiyama T.,
RA   Aoki S., Wada K., Kiyama H.;
RT   "Damage-induced neuronal endopeptidase (DINE) is a unique
RT   metallopeptidase expressed in response to neuronal damage and
RT   activates superoxide scavengers.";
RL   Proc. Natl. Acad. Sci. U.S.A. 97:4345-4350(2000).
RN   [2]
RP   SEQUENCE OF 431-632 FROM N.A.
RX   MEDLINE=99132387; PubMed=9931490;
RA   Valdenaire O., Richards J.G., Faull R.L.M., Schweizer A.;
RT   "XCE, a new member of the endothelin-converting enzyme and neutral
RT   endopeptidase family, is preferentially expressed in the CNS.";
RL   Brain Res. Mol. Brain Res. 64:211-221(1999).
CC   -!- FUNCTION: May contribute to the degradation of peptide hormones
CC       and be involved in the inactivation of neuronal peptides. Cleaves
CC       the synthetic substrate Z-Gly-Gly-Leu-pNA and releases pNA. May
CC       protect against C2-ceramide-induced apoptosis.
CC   -!- COFACTOR: Binds 1 zinc ion (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein.
CC   -!- TISSUE SPECIFICITY: Highly expressed in the CNS, in particular in
CC       neurons of the caudate putamen, diagonal band, the paraventricular
CC       nucleus of the thalamus, part of the hypothalamus, in cranial
CC       motor nuclei, inferior olive, and substantia gelatinosa of the
CC       spinal tract trigeminal nucleus. Not detected in cerebral cortex,
CC       hippocampus and cerebellum.
CC   -!- INDUCTION: By mechanical damage to nerve cells.
CC   -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M13.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AB026293; BAA95004.1; -.
DR   EMBL; AB023896; BAA95006.1; -.
DR   EMBL; Y16188; CAA76114.1; -.
DR   HSSP; P08473; 1DMT.
DR   MEROPS; M13.007; -.
DR   InterPro; IPR000718; Peptidase_M13.
DR   InterPro; IPR000130; Zn_MTpeptdse.
DR   Pfam; PF01431; Peptidase_M13; 1.
DR   PRINTS; PR00786; NEPRILYSIN.
DR   PROSITE; PS00142; ZINC_PROTEASE; 1.
KW   Hydrolase; Protease; Metalloprotease; Metal-binding; Zinc;
KW   Glycoprotein; Transmembrane; Signal-anchor.
FT   DOMAIN        1     61       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     62     82       SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT                                (POTENTIAL).
FT   DOMAIN       83    775       LUMENAL (POTENTIAL).
FT   METAL       612    612       ZINC (CATALYTIC) (BY SIMILARITY).
FT   ACT_SITE    613    613       BY SIMILARITY.
FT   METAL       616    616       ZINC (CATALYTIC) (BY SIMILARITY).
FT   METAL       672    672       ZINC (CATALYTIC) (BY SIMILARITY).
FT   CARBOHYD    255    255       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    322    322       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    656    656       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT    536    536       L -> F (IN REF. 2).
SQ   SEQUENCE   775 AA;  87944 MW;  0823091F98A41556 CRC64;

  Query Match             24.7%;  Score 977;  DB 1;  Length 775;
  Best Local Similarity   30.5%;  Pred. No. 4e-58;
  Matches  239;  Conservative  158;  Mismatches  293;  Indels   94;  Gaps   22;

Qy      11 TGKKANRGTRIAL-------VVFVGGTLVLGTILFLVSQGLLSLQ----------AKQE 52
           :|: |: | |  |         |  : | ||    |  :   :|:|:          | |
Db      41 SGRSAS-GARSGLPRWNRREVCLLSG-LVFAAGLCAILAAMLALKYLGPGAAGTGGACPE 98

Qy      53 YCLKPECIEAAAAILS-KVNLSVDPCDNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNV 111
           | : :    ||  ||  :: |:||| :|: ||| ||:  : ||:|  :||   :
Db      99 GCPERKAFARAARFLSANLDASIDPCQDFYSFACGGWLRRHAIPDDKLTYGTIAAIGEQN 158

Qy     112 DLKLKELLEKSISRRRDT-----EAIQKAKILYSSCMNEKAIEKADAKPLLHILRHSPFR 166
           : :|: ||          | |       | :| :  : ||:: : ||:   :|:| ::
Db     159 EERLRRLL------ARPTGGPGGAAQRKVRAFFRSCLDMREIERLGPRPMLEVIEDC--- 209

Qy     167 WPVLESNIGPEGVW---------SERKFSLLQTLATFRGQYSNSVFIRLYVSPDDKASNE 217
                 | |                :: | : |   :| || :    | || ||: |:
Db     210 ----------GGWDLGGAADRPGAARWDLNRLLYKAQGVYSAAALFSLTVSLDDRNSSR 258

Qy     218 HILKLDQATLSLAVREDYLDNSTEAKSYRDALYKFMVDTAVLLGANSSRAEHDMKSVLRL 277
           :::::||  |:|  |  ||     ::    |  ||          ||||::   |   : :|:|
Db     259 YVIRIDQDGLTLPERTLYLAQDEGSEKVLAAYKVFMERLLRLLGADA--VEQKAQEILQL 316

Qy     278 EIKIAEIMIPHEN---RTSEAMYNKMNISELSAMIPQFDWLGYIKKVIDTRLYPHLKDIS 334
           | ::| | :   :   |   ::|||: : :|  : |   |   : ::          :| |
Db     317 EQRLANISVSEYDDLRRDVSSVYNKVTLGQLQKITPHLQWKWLLDQIFQ-------EDFS 369

Qy     335 PSENVVVRVPQYFKDLFRILGSERKKTIANYLVWRMVYSRIPNLSRRFQYRWLEFSRVIQ 394
           | ||:    | : : ::: |  :: : ||||||:|        :||  |:    | :: ::
Db     370 EEEEVVLLATDYMQQVSQLIRSTPRRILHNYLVWRVVVVLSEHLSPPFREALHELAKEME 429

Qy     395 GTTTLLPQWDK-------CVNFIESALPYVVGKMFVDVYFQEDKKEMMEELVEGVRWAFI 447
           |        ||       |:          :| :||  :|    |  :::||| :::
Db     430 GN-------DKPQELARVCLGQANRHFGMALGALFVHEHFSAASKAKVQQLVEDIKYILG 482

Qy     448 DMLEKENEWMDAGTKRKAKEKARAVLAKVGYPEFIMNDTHVNEDLKAIKFSEADYFGNVL 507
           || | :|||| ||  |: | : ::  ||||:|::    |::: :  :  |  |  |:|
Db     483 QRLE-ELDWMDAQTKAAARAKLQYMMVMVGYPDFLLKPEAVDKEYE-FEVHEKTYLKNIL 540

Qy     508 QTRKYLAQSDFFWLRKAVPKTEWFTNPTTVNAFYSASTNQIRFPAGELQKPFFWGTEYPR 567
           : ::  |     :|: | |: |   |  :||:|  : ||: |||| || |  :  ::|:
Db     541 NSIRFSIQLSVKKIRQEVDKSTWLLPPQALNAYYLPNKNQMVFPAGILQ-PTLYDPDFPQ 599

Qy     568 SLSYGAIGVIVGHEFTHGFDNNGRKYDKNGNLDPWWSTESEEKFKEKTKCMINQYSNY-- 625
           ||:|| || |:||| |||:|: | :||::|||  ||:  |  :|  | :|::  | |:
Db     600 SLNYGGIGTIIGHELTHGYDDWGGQYDRSGNLLHWWTEASYSRFLHKAECIVRLYDNFTV 659

Qy     626 YWKKAGLNVKGKRTLGENIADNGGLREAFRAYRKWINDRRQGLEEPLLPGITFTNNQLFF 685
           | ::    | || |||||||| |||: |: ||:||:  |  | | | |  : :|:||||
Db     660 YNQR----VNGKHTLGENIADMGGLKLAYYAYQKWV--REHGPEHP-LHRLKYTHNQLFF 712

Qy     686 LSYAHVRCNSYRPEAAREQVQIGAHSPPQFRVNGAISNSEEFQKAFNCPPNSTMNRGMDS 745
           :::|   |   | ::   ||    |:|  :|| |::|  ||| :||:|| :| ||  :
Db     713 IAFAQNWCIKRRSQSIYLQVLTDKHAPEHYRVLGSVSQFEEFGRAFHCPKDSPMN-PVHK 771

Qy     746 CRLW 749
           | :|
Db     772 CSVW 775


RESULT 15
ECEL_HUMAN
ID   ECEL_HUMAN     STANDARD;      PRT;   775 AA.
AC   O95672; Q9NY95;
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Endothelin-converting enzyme-like 1 (EC 3.4.24.-) (Xce protein).
GN   ECEL1 OR XCE.
```

```
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Caudate, and Spinal cord;
RX   MEDLINE=99132387; PubMed=9931490;
RA   Valdenaire O., Richards J.G., Faull R.L.M., Schweizer A.;
RT   "XCE, a new member of the endothelin-converting enzyme and neutral
RT   endopeptidase family, is preferentially expressed in the CNS.";
RL   Brain Res. Mol. Brain Res. 64:211-221(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20164043; PubMed=10698686;
RA   Valdenaire O., Rohrbacher E., Langeveld A., Schweizer A., Meijers C.;
RT   "Organization and chromosomal localization of the human ECEL1 (XCE)
RT   gene encoding a zinc metallopeptidase involved in the nervous control
RT   of respiration.";
RL   Biochem. J. 346:611-616(2000).
CC   -!- FUNCTION: May contribute to the degradation of peptide hormones
CC       and be involved in the inactivation of neuronal peptides.
CC   -!- COFACTOR: Binds 1 zinc ion (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein (By similarity).
CC   -!- TISSUE SPECIFICITY: Highly expressed in the CNS, in particular in
CC       putamen, spinal cord, medulla and subthalamic nucleus. A strong
CC       signal was also detected in uterine subepithelial cells and around
CC       renal blood vessels. Detected at lower levels in amygdala,
CC       caudate, thalamus, pancreas and skeletal muscle. Detected at very
CC       low levels in substantia nigra, cerebellum, cortex, corpus
CC       callosum and hippocampus.
CC   -!- PTM: N-glycosylated.
CC   -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M13.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Y16187; CAA76113.1; -.
DR   EMBL; AJ130734; CAB86601.1; -.
DR   HSSP; P08473; 1DMT.
DR   MEROPS; M13.007; -.
DR   Genew; HGNC:3147; ECEL1.
DR   MIM; 605896; -.
DR   InterPro; IPR000718; Peptidase_M13.
DR   InterPro; IPR001230; Prenyl_site.
DR   InterPro; IPR000130; Zn_MTpeptdse.
DR   Pfam; PF01431; Peptidase_M13; 1..
DR   PRINTS; PR00786; NEPRILYSIN.
DR   PROSITE; PS00142; ZINC_PROTEASE; 1.
KW   Hydrolase; Protease; Metalloprotease; Metal-binding; Zinc;
KW   Glycoprotein; Transmembrane; Signal-anchor; Polymorphism.
FT   DOMAIN        1     59       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     60     82       SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT                                (POTENTIAL).
FT   DOMAIN       83    775       LUMENAL (POTENTIAL).
FT   METAL       612    612       ZINC (CATALYTIC) (BY SIMILARITY).
FT   ACT_SITE    613    613       BY SIMILARITY.
FT   METAL       616    616       ZINC (CATALYTIC) (BY SIMILARITY).
FT   METAL       672    672       ZINC (CATALYTIC) (BY SIMILARITY).
FT   CARBOHYD    255    255       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    322    322       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    656    656       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARIANT      10     10       H -> Q (IN DBSNP:2741281).
FT                                /FTId=VAR_012813.
FT   VARIANT     328    328       Y -> H (IN DBSNP:1529874).
FT                                /FTId=VAR_012814.
FT   CONFLICT    286    286       V -> I (IN REF. 2).
FT   CONFLICT    757    758       VL -> AF (IN REF. 2).
FT   CONFLICT    763    763       V -> D (IN REF. 2).
SQ   SEQUENCE   775 AA;  87781 MW;  5B43E0FE11C5B55C CRC64;

  Query Match           24.5%;  Score 969.5;  DB 1;  Length 775;
  Best Local Similarity   30.7%;  Pred. No. 1.3e-57;
  Matches  231;  Conservative  157;  Mismatches  297;  Indels   67;  Gaps   19;

Qy      23 LVVFVGGTLVLGTILFLVSQGLLSL--QAKQEYCLKPECIEAAAAIL-SKVNLSVDPCDN 79
           ||   |  :|  :| |   | ::    |  | | : :    ||  | : :: |:||| :
Db      66 LVFAAGLCAILAAMLALKYLGPVAAGGGACPEGCPERKAFARAARFLAANLDASIDPCQD 125

Qy      80 FFRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLEKSISRRRDTEAIQKAKILY 139
           |: ||| ||:  : ||:|  :||    :   : :|: || :          | :| :  :
Db     126 FYSFACGGWLRRHAIPDDKLTYGTIAAIGEQNEERLRRLLARP-GGGPGGAAQRKVRAFF 184

Qy     140 SSCMNEKAIEKADAKPLLHILRHSPFRWPVLESNIGPEGVW-----SER-----KFSLLQ 189
           ||:: : ||:   :|:| ::                  | |       ||      :: | :
Db     185 RSCLDMREIERLGPRPMLEVIEDC-------------GGWDLGGAEERPGVAARWDLNR 230

Qy     190 TLATFRGQYSNSVFIRLYVSPDDKASNEHILKLDQATLSLAVREDYLDNSTEAKSYRDAL 249
           |   :| || :    | || ||: |: :::::|| |:|  |  ||    :::     |
Db     231 LLYKAQGVYSAAALFSLTVSLDDRNSSRYVIRIDQDGLTLPERTLYLAQDEDSEKVLAAY 290

Qy     250 YKFMVDTAVLLGANSSRAEHDMKSVLRLEIKIAEIMIPHEN---RTSEAMYNKMNISELS 306
             ||     ||||::   |   : :|::| ::| | :   :   |   :||||: : :|
Db     291 RVFMERVLSLLGADA--VEQKAQEILQVEQQLANITVSEYDDLRRDVSSMYNKVTLGQLQ 348

Qy     307 AMIPQFDWLGYIKKVIDTRLYPHLKDISPSENVVVRVPQYFKDLFRILGSERKKTIANYL 366
           : |  |  : ::          :| |  | ||:    | : : ::: |   : : |||
Db     349 KITPHLRWKWLLDQIFQ-------EDFSEEEEVVLLATDYMQQVSQLIRSTPHRVLHNYL 401

Qy     367 VWRMVYSRIPNLSRRFQYRWLEFSRVIQGTTTLLPQWDK-------CVNFIESALPYVVG 419
           |||:|     :||  |:    | :: ::|:          ||       |:         :|
Db     402 VWRVVVVLSEHLSPPFREALHELAQEMEGS-------DKPQELARVCLGQANRHFGMALG 454

Qy     420 KMFVDVYFQEDKKEMMEELVEGVRWAFIDMLEKENEWMDAGTKRKAKEKARAVLAKVGYP 479
           :||  :|    |  :::||| :::     || | :|||| |:  |: | : ::  ||||
Db     455 ALFVHEHFSAASKAKVQQLVEDIKYILGQRLE-ELDWMDAETRAAARAKLQYMMVMVGYP 513

Qy     480 EFIMNDTHVNEDLKAIKFSEADYFGNVLQTRKYLAQSDFFWLRKAVPKTEWFTNPTTVNA 539
           :|::    |::: :  :  |  || |:| : ::  |     :|: | |: |   | :||
Db     514 DFLLKPDAVDKEYE-FEVHEKTYFKNILNSIRFSIQLSVKKIRQEVDKSTWLLPPQALNA 572

Qy     540 FYSASTNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNGRKYDKNGNL 599
           :|  : ||: |||| || |  :  ::|:||:|| || |:||| |||:|: | :|||:|||
Db     573 YYLPNKNQMVFPAGILQ-PTLYDPDFPQSLNYGGIGTIIGHELTHGYDDWGGQYDRSGNL 631

Qy     600 DPWWSTESEEKFKEKTKCMINQYSNY--YWKKAGLNVKGKRTLGENIADNGGLREAFRAY 657
             ||:  |  :|  | :|::  | |:  | ::    | || |||||||| |||: |: ||
Db     632 LHWWTEASYSRFLRKAECIVRLYDNFTVYNQR----VNGKHTLGENIADMGGLKLAYHAY 687

Qy     658 RKWINDRRQGLEEPLLPGITFTNNQLFFLSYAHVRCNSYRPEAAREQVQIGAHSPPQFRV 717
           :||:  |  | | | || : :|::||||:::|   |   | ::   ||    |:|  :||
Db     688 QKWV--REHGPEHP-LPRLKYTHDQLFFIAFAQNWCIKRRSQSIYLQVLTDKHAPEHYRV 744

Qy     718 NGAISNSEEFQKAFNCPPNSTMNRGMDSCRLW 749
           |::|  ||| :  :||  | ||     | :|
Db     745 LGSVSQFEEFGRVLHCPKVSPMNPA-HKCSVW 775


Search completed: May 21, 2003, 18:48:18
Job time : 31 secs
```

GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

Run on: May 21, 2003, 18:44:34 ; Search time 41 Seconds
(without alignments)
3764.129 Million cell updates/sec

Title: US-09-913-955A-1
Perfect score: 3958
Sequence: 1 MEAETGSSVETGKKANRGTR.....AFNCPPNSTMNRGMDSCRLW 749

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3819	96.5	749	11	O35812	O35812 rattus norv
2	1380	34.9	742	11	Q9ERK3	Q9erk3 mus musculu
3	1375.5	34.8	765	11	Q9JLI3	Q9jli3 mus musculu
4	1373	34.7	742	11	Q9QZV6	Q9qzv6 mus musculu
5	1368.5	34.6	765	11	Q9QZV7	Q9qzv7 mus musculu
6	1361.5	34.4	779	11	Q9ERK2	Q9erk2 mus musculu
7	1335	33.7	770	13	O93394	O93394 perca flave
8	1332.5	33.7	770	4	Q96PH9	Q96ph9 homo sapien
9	1257	31.8	752	13	Q9DGN6	Q9dgn6 gallus gall
10	1253.5	31.7	758	6	Q28868	Q28868 bos taurus
11	1248.5	31.5	758	6	Q28010	Q28010 bos taurus
12	1223	30.9	787	5	Q9UA44	Q9ua44 aplysia cal
13	1219	30.8	772	5	Q9BLH1	Q9blh1 bombyx mori
14	1209	30.5	848	5	O16796	O16796 caenorhabdi
15	1208	30.5	763	11	Q923T6	Q923t6 mus musculu
16	1205.5	30.5	661	5	Q9W435	Q9w435 drosophila
17	1187.5	30.0	1040	5	Q8T062	Q8t062 drosophila
18	1182	29.9	770	5	Q9U9P2	Q9u9p2 hydra atten
19	1153.5	29.1	786	5	Q8SWS1	Q8sws1 drosophila
20	1150.5	29.1	726	5	Q9W5Y0	Q9w5y0 drosophila
21	1134.5	28.7	736	5	O44857	O44857 caenorhabdi
22	1119	28.3	763	5	Q9XZ01	Q9xz01 drosophila
23	1117.5	28.2	739	5	Q8T660	Q8t660 venturia ca
24	1014.5	25.6	766	5	Q18673	Q18673 caenorhabdi
25	911	23.0	677	5	Q9I7I4	Q9i7i4 drosophila
26	822	20.8	665	17	Q8TPB2	Q8tpb2 methanosarc
27	814.5	20.6	706	16	Q9A2Q2	Q9a2q2 caulobacter
28	798	20.2	689	2	O50642	O50642 porphyromon
29	778	19.7	754	5	Q19831	Q19831 caenorhabdi
30	691	17.5	167	13	O93586	O93586 gallus gall
31	672	17.0	663	16	O53649	O53649 mycobacteri
32	668	16.9	700	16	Q9PFT1	Q9pft1 xylella fas
33	653.5	16.5	683	5	Q9Y136	Q9y136 drosophila
34	646.5	16.3	667	16	O06075	O06075 mycobacteri
35	643.5	16.3	700	5	Q9VAS0	Q9vas0 drosophila
36	607	15.3	717	5	Q9VAY0	Q9vay0 drosophila
37	606	15.3	1589	5	O45569	O45569 caenorhabdi
38	588.5	14.9	756	5	Q8WSK6	Q8wsk6 dermacentor
39	586	14.8	713	11	Q9EQF2	Q9eqf2 mus musculu
40	584	14.8	870	5	Q9GTJ6	Q9gtj6 ancylostoma
41	571	14.4	648	2	Q8VTS9	Q8vts9 lactobacill
42	567	14.3	798	5	Q22763	Q22763 caenorhabdi
43	561.5	14.2	681	5	Q9VAS4	Q9vas4 drosophila
44	558.5	14.1	823	5	O45131	O45131 haemonchus
45	554	14.0	507	5	Q9GTJ5	Q9gtj5 ancylostoma

ALIGNMENTS

RESULT 1
O35812
ID O35812 PRELIMINARY; PRT; 749 AA.
AC O35812;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE PHEX protein.
GN PHEX.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=INCISOR;
RX MEDLINE=97343325; PubMed=9199930;
RA Francis F., Strom T.M., Hennig S., Boeddrich A., Lorenz B.,
RA Brandau O., Mohnike K.L., Cagnoli M., Steffens C., Klages S.,
RA Borzym K., Pohl T., Oudet C., Econs M.J., Rowe P.S., Reinhardt R.,
RA Meitinger T., Lehrach H.;
RT "Genomic organization of the human PEX gene mutated in X-linked
RT dominant hypophosphatemic rickets.";
RL Genome Res. 7:573-585(1997).
DR EMBL; AJ001637; CAA04890.1; -.
DR HSSP; P08473; 1DMT.
DR MEROPS; M13.091; -.
DR InterPro; IPR000718; Peptidase_M13.
DR InterPro; IPR001230; Prenyl_site.
DR InterPro; IPR000130; Zn_MTpeptdse.
DR Pfam; PF01431; Peptidase_M13; 1.
DR PRINTS; PR00786; NEPRILYSIN.
DR PROSITE; PS00294; PRENYLATION; UNKNOWN_1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
SQ SEQUENCE 749 AA; 86305 MW; 690B8E82609C1A63 CRC64;

Query Match 96.5%; Score 3819; DB 11; Length 749;
Best Local Similarity 95.3%; Pred. No. 3.1e-256;
Matches 714; Conservative 22; Mismatches 13; Indels 0; Gaps 0;

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Qy       1 MEAETGSSVETGKKANRGTRIALVVFVGGTLVLGTILFLVSQGLLSLQAKQEYCLKPECI 60
Db       1 MEAEAGSTMETGKGTNRGIRIALALFITGTLVLGTLLFLVSQGLLSFQAKQEYCLKPECI 60

Qy      61 EAAAAILSKVNLSVDPCDNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLE 120
Db      61 EAAAAIMSKVNLSVDPCENFFRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKALLE 120

Qy     121 KSISRRRDTEAIQKAKILYSSCMNEKAIEKADAKPLLHILRHSPFRWPVLESNIGPEGVW 180
Db     121 KSVSRRRDTEAVQKAKILYSSCMNEKAIEKADAKPLLHILRHSPFRWPVLEANIGPEGVW 180

Qy     181 SERKFSLLQTLATFRGQYSNSVFIRLYVSPDDKASNEHILKLDQATLSLAVREDYLDNST 240
Db     181 SERKFSLLQTLATFRGQYSNSVFIRLYVSPDDKASNEHILKLDQATLSLAVREDFLDNTT 240

Qy     241 EAKSYRDALYKFMVDTAVLLGANSSRAEHDMKSVLRLEIKIAEIMIPHENRTSEAMYNKM 300
Db     241 EAKSYRDALYKFMVDTAVLLGANSSRAEHDMKSVLRLEIKIAEIMIPHENRTSEAMYNKM 300

Qy     301 NISELSAMIPQFDWLGYIKKVIDTRLYPHLKDISPSENVVVRVPQYFKDLFRILGSERKK 360
Db     301 NISELSAMIPQFDWLGYIKKVIDTRLYPHLKDIGPSENVVVRVPQYFKDLFRILGAERKK 360

Qy     361 TIANYLVWRMVYSRIPNLSRRFQYRWLEFSRVIQGTTTLLPQWDKCVNFIESALPYVVGK 420
Db     361 TIANYLVWRMVYSRIPNLSRRFQYRWLEFSRVIQGTTTLLPQWDKCVNFIESALPYVVGK 420

Qy     421 MFVDVYFQEDKKEMMEELVEGVRWAFIDMLEKENEWMDAGTKRKAKEKARAVLAKVGYPE 480
Db     421 MFVNVHFQEDKKEMMEELIEGVRWAFIDMLEKENEWMDAGTKRKAQEKARAVLAKVGYPE 480

Qy     481 FIMNDTHVNEDLKAIKFSEADYFGNVLQTRKYLAQSDFFWLRKAVPKTEWFTNPTTVNAF 540
Db     481 FIMNDTYVNEDLKAIKFSESDYFGNVLQTRKYLAQSDFFWLKKAVPKTEWFTNPTTVNAF 540

Qy     541 YSASTNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNGRKYDKNGNLD 600
Db     541 YSASTNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNGRKYDKNGNLD 600

Qy     601 PWWSTESEEKFKEKTKCMINQYSNYYWKKAGLNVKGKRTLGENIADNGGLREAFRAYRKW 660
Db     601 PWWSVDSEEKFKEKTKCMINQYSNYYWKKAGLNVKGKRTLGENIADNGGLREAFRAYRKW 660

Qy     661 INDRRQGLEEPLLPGITFTNNQLFFLSYAHVRCNSYRPEAAREQVQIGAHSPPQFRVNGA 720
Db     661 INDRRQGVEEPLLPGITFTNNQLFFLSYAHVRCNSYRPEAAREQVQIGAHSPPQFRVNGA 720

Qy     721 ISNSEEFQKAFNCPPNSTMNRGMDSCRLW 749
Db     721 ISNFEEFQKAFNCPANSTMNRGADSCRLW 749
```

RESULT 2
Q9ERK3
ID   Q9ERK3   PRELIMINARY;   PRT;   742 AA.
AC   Q9ERK3;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Neprilysin-like peptidase alpha.
GN   MELL1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21293028; PubMed=11278416;
RA   Shirotani K., Tsubuki S., Iwata N., Takaki Y., Harigaya W.,
RA   Maruyama K., Kiryu-Seo S., Kiyama H., Iwata H., Tomita T.,
RA   Iwatsubo T., Saido T.C.;
RT   "Neprilysin Degrades Both Amyloid beta Peptides 1-40 and 1-42 Most
RT   Rapidly and Efficiently among Thiorphan- and Phosphoramidon-sensitive
RT   Endopeptidases.";
RL   J. Biol. Chem. 276:21895-21901(2001).
DR   EMBL; AF302075; AAG18446.1; -.
DR   HSSP; P08473; 1DMT.
DR   MEROPS; M13.008; -.
DR   MGD; MGI:1351603; Mell1.
DR   InterPro; IPR000718; Peptidase_M13.
DR   InterPro; IPR001230; Prenyl_site.
DR   InterPro; IPR000130; Zn_MTpeptdse.
DR   Pfam; PF01431; Peptidase_M13; 1.
DR   PRINTS; PR00786; NEPRILYSIN.
DR   PROSITE; PS00294; PRENYLATION; UNKNOWN_1.
DR   PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
SQ   SEQUENCE   742 AA; 85993 MW; 4A44EAD211B2499F CRC64;

Query Match 34.9%; Score 1380; DB 11; Length 742;
Best Local Similarity 38.8%; Pred. No. 3.6e-87;
Matches 291; Conservative 148; Mismatches 267; Indels 44; Gaps 17;

```
Qy      18 GTRIALVVFVGGTLVLGTILFLVSQGLLSLQAKQEYCLKPECIEAAAAILSKVNLSVDPC 77
Db      19 GLMVLLLLLLGAIVTLGV---FYSIALRDSSLKSDICTTPSCVIAAARILENMDQSRNPC 75

Qy      78 DNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLEKSISRRRDTEAIQKAKI 137
Db      76 ENFYQYACGGWLRHHVIPETNSRYSVFDILRDELEVILKGVLEDSTSQHR--PAVEKAKT 133

Qy     138 LYSSCMNEKAIEKADAKPLLHILRHSPFRWPVLESNIGPEGVWSER---KFSLLQTLATF 194
Db     134 LYRSCMNQSVIEKRDSEPLLSVLK-MVGGWPVAMDK------WNETMGLKWELERQLAVL 186

Qy     195 RGQYSNSVFIRLYVSPDDKASNEHILKLDQATLSLAVREDYLDNSTEAKSYRDALYKFMV 254
Db     187 NSQFNRRVLIDLFIWNDDQNSSRHVIYIDQPTLGMPSREYYFQEDNNHK-VRKAYLEFMT 245

Qy     255 DTAVL------LGANSSRAEHDMKSVLRLEIKIAEIMIPHENRTS-EAMYNKMNISELSA 307
Db     246 SVATMLRKDQNLSKESAMVREEMAEVLELETHLANATVPQEKRHDVTALYHRMDLMELQE 305

Qy     308 M--IPQFDWLGYIKKV---IDTRLYPHLKDISPSENVVVRVPQYFKDLFRILGSERKKTI 362
Db     306 RFGLKGFNWTLFIQNVLSSVEVELF-------PDEEVVVYGIPYLENLEDIIDSYSARTM 358

Qy     363 ANYLVWRMVYSRIPNLSRRFQYRWLEFSRVIQGTTTLLPQWDKCVNFIESALPYVVGKMF 422
Db     359 QNYLVWRLVLDRIGSLSQRFKEARVDYRKALYGTTVEEVRWRECVSYVNSNMESAVGSLY 418

Qy     423 VDVYFQEDKKEMMEELVEGVRWAFIDMLEKENEWMDAGTKRKAKEKARAVLAKVGYPEFI 482
Db     419 IKRAFSKDSKSTVRELIEKIRSVFVDNLDELN-WMDEESKKKAQEKAMNIREQIGYPDYI 477

Qy     483 M--NDTHVNEDLKAIKFSEADYFGNVLQTRKYLAQSDFFWLRKAVPKTEWFTNPTTVNAF 540
Db     478 LEDNNKHLDEEYSSLTFYEDLYFENGLQNLKNNAQRSLKKLREKVDQNLWIIGAAVVNAF 537

Qy     541 YSASTNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNGRKYDKNGNLD 600
Db     538 YSPNRNQIVFPAGILQPPFF-SKDQPQSLNFGGIGMVIGHEITHGFDDNGRNFDKNGNML 596

Qy     601 PWWSTESEEKFKEKTKCMINQYSNYYWKKA-GLNVKGKRTLGENIADNGGLREAFRAYRK 659
Db     597 DWWSNFSARHFQQQSQCMIYQYGNFSWELADNQNVNGFSTLGENIADNGGVRQAYKAYLR 656

Qy     660 WINDRRQGLEEPLLPGITFTNNQLFFLSYAHVRCNSYRPEAAREQVQIGAHSPPQFRVNG 719
Db     657 WLAD---GGKDQRLPGLNLTYAQLFFINYAQVWCGSYRPEFAVQSIKTDVHSPLKYRVLG 713

Qy     720 AISNSEEFQKAFNCPPNSTMNRGMDSCRLW 749
Db     714 SLQNLPGFSEAFHCPRGSPMH-PMKRCRIW 742
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```
RESULT 3
Q9JLI3
ID   Q9JLI3      PRELIMINARY;      PRT;   765 AA.
AC   Q9JLI3;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Neprilysin-like metallopeptidase 1 (Neprilysin-like peptidase
DE   beta).
GN   MELL1 OR SEP OR NL1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=TESTIS;
RX   PubMed=10749671;
RA   Ghaddar G., Ruchon A.F., Carpentier M., Marcinkiewicz M., Seidah N.G.,
RA   Crine P., DesGroseillers L., Boileau G.;
RT   "Molecular cloning and biochemical characterization of a new mouse
RT   testis soluble zinc-metallopeptidase of the neprilysin family.";
RL   Biochem. J. 347:419-429(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Shirotani K., Saido T.C.;
RT   "Cloning of neprilysin-like peptidase cDNAs.";
RL   Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF176569; AAF69247.1; -.
DR   EMBL; AF302076; AAG18447.1; -.
DR   HSSP; P08473; 1DMT.
DR   MEROPS; M13.008; -.
DR   MGD; MGI:1351603; Mell1.
DR   InterPro; IPR000718; Peptidase_M13.
DR   InterPro; IPR001230; Prenyl_site.
DR   InterPro; IPR000130; Zn_MTpeptdse.
DR   Pfam; PF01431; Peptidase_M13; 1.
DR   PRINTS; PR00786; NEPRILYSIN.
DR   PROSITE; PS00294; PRENYLATION; UNKNOWN_1.
DR   PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
SQ   SEQUENCE   765 AA;  88699 MW;  D3662F1CE5B957F7 CRC64;

  Query Match             34.8%;  Score 1375.5;  DB 11;  Length 765;
  Best Local Similarity   38.8%;  Pred. No. 7.7e-87;
  Matches  295;  Conservative  147;  Mismatches  267;  Indels   51;  Gaps   18;

Qy      18 GTRIALVVF--VGGTLVLGTILF--------LVSQGLLSLQAKQEYCLKPECIEAAAAIL 67
           |  : | ||  :|  | | | |          :| : |     | : |  | |: ||| ||
Db      29 GAIVTLGVFYSIGKQLPLLTSLLHFSWDERTVVKRALRDSSLKSDICTTPSCVIAAARIL 88

Qy      68 SKVNLSVDPCDNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLEKSISRRR 127
           :: | :||:||:::|| ||: :: |||    | |:  ||  ::: || :|| | |: |
Db      89 ENMDQSRNPCENFYQYACGGWLRHHVIPETNSRYSVFDILRDELEVILKGVLEDSTSQHR 148

Qy     128 DTEAIQKAKILYSSCMNEKAIEKADAKPLLHILRHSPFRWPVLESNIGPEGVWSER---K 184
           |::||| || ||||:  ||| |::||| :|:     |||           |:|    |
Db     149 --PAVEKAKTLYRSCMNQSVIEKRDSEPLLSVLK-MVGGWPVAMDK------WNETMGLK 199

Qy     185 FSLLQTLATFRGQYSNSVFIRLYVSPDDKASNEHILKLDQATLSLAVREDYLDNSTEAKS 244
           : | : ||    |::  | | |::  ||: |: |:: :|| || :  || |       |
Db     200 WELERQLAVLNSQFNRRVLIDLFIWNDDQNSSRHVIYIDQPTLGMPSREYYFQEDNNHK- 258

Qy     245 YRDALYKFMVDTAVL------LGANSSRAEHDMKSVLRLEIKIAEIMIPHENRTS-EAMY 297
           | |  :||   | :       |   |:    :|  || ||  :|   :| | |    |:|
Db     259 VRKAYLEFMTSVATMLRKDQNLSKESAMVREEMAEVLELETHLANATVPQEKRHDVTALY 318

Qy     298 NKMNISELSAM--IPQFDWLGYIKKV---IDTRLYPHLKDISPSENVVVRVPQYFKDLFR 352
           ::|:: ||     :  |:|  :|: |   ::  |:       | | |||    | ::|
Db     319 HRMDLMELQERFGLKGFNWTLFIQNVLSSVEVELF-------PDEEVVVYGIPYLENLED 371

Qy     353 ILGSERKKTIANYLVWRMVYSRIPNLSRRFQYRWLEFSRVIQGTTTLLPQWDKCVNFIES 412
           |: |   :|: ||||||:|  || :||:||:   ::: : : |||    :| :||::: |

Db     372 IIDSYSARTMQNYLVWRLVLDRIGSLSQRFKEARVDYRKALYGTTVEEVRWRECVSYVNS 431

Qy     413 ALPYVVGKMFVDVYFQEDKKEMMEELVEGVRWAFIDMLEKENEWMDAGTKRKAKEKARAV 472
             :   || :::   | :| | : ||:| :|  |:| |:: | |||  :|:||:|||  :
Db     432 NMESAVGSLYIKRAFSKDSKSTVRELIEKIRSVFVDNLDELN-WMDEESKKKAQEKAMNI 490

Qy     473 LAKVGYPEFIM--NDTHVNEDLKAIKFSEADYFGNVLQTRKYLAQSDFFWLRKAVPKTEW 530
             ::|||::|:  |: |::|:  :: | |  || | ||  |  ||     ||: | :  |
Db     491 REQIGYPDYILEDNNKHLDEEYSSLTFYEDLYFENGLQNLKNNAQRSLKKLREKVDQNLW 550

Qy     531 FTNPTTVNAFYSASTNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNG 590
                 |||||| : ||| |||| || |||   : |:||::| ||:::||| |||||:||
Db     551 IIGAAVVNAFYSPNRNQIVFPAGILQPPFF-SKDQPQSLNFGGIGMVIGHEITHGFDDNG 609

Qy     591 RKYDKNGNLDPWWSTESEEKFKEKTKCMINQYSNYYWKKA-GLNVKGKRTLGENIADNGG 649
           | :|||||:  |||  |   |:::::||| || |: |: |   || |  ||||||||||||
Db     610 RNFDKNGNMLDWWSNFSARHFQQQSQCMIYQYGNFSWELADNQNVNGFSTLGENIADNGG 669

Qy     650 LREAFRAYRKWINDRRQGLEEPLLPGITFTNNQLFFLSYAHVRCNSYRPEAAREQVQIGA 709
           :|:|::|| :|: |   | ::  |||:  |  ||||::|| | | ||||| | : ::
Db     670 VRQAYKAYLRWLAD---GGKDQRLPGLNLTYAQLFFINYAQVWCGSYRPEFAVQSIKTDV 726

Qy     710 HSPPQFRVNGAISNSEEFQKAFNCPPNSTMNRGMDSCRLW 749
           ||| ::|| |:: |   | :||:||  | |:  |  ||:|
Db     727 HSPLKYRVLGSLQNLPGFSEAFHCPRGSPMH-PMKRCRIW 765


RESULT 4
Q9QZV6
ID   Q9QZV6      PRELIMINARY;      PRT;   742 AA.
AC   Q9QZV6;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Soluble secreted endopeptidase delta.
GN   MELL1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20011457; PubMed=10542292;
RA   Ikeda K., Emoto N., Raharjo S.B., Nurhantari Y., Saiki K.,
RA   Yokoyama M., Matsuo M.;
RT   "Molecular identification and characterization of novel membrane-bound
RT   metalloprotease, the soluble secreted form of which hydrolyzes a
RT   variety of vasoactive peptides.";
RL   J. Biol. Chem. 274:32469-32477(1999).
DR   EMBL; AF157106; AAF13153.1; -.
DR   HSSP; P08473; 1DMT.
DR   MEROPS; M13.008; -.
DR   MGD; MGI:1351603; Mell1.
DR   InterPro; IPR000718; Peptidase_M13.
DR   InterPro; IPR001230; Prenyl_site.
DR   InterPro; IPR000130; Zn_MTpeptdse.
DR   Pfam; PF01431; Peptidase_M13; 1.
DR   PRINTS; PR00786; NEPRILYSIN.
DR   PROSITE; PS00294; PRENYLATION; UNKNOWN_1.
DR   PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
SQ   SEQUENCE   742 AA;  85945 MW;  CF5FF9D982471157 CRC64;

  Query Match             34.7%;  Score 1373;  DB 11;  Length 742;
  Best Local Similarity   38.7%;  Pred. No. 1.1e-86;
  Matches  290;  Conservative  149;  Mismatches  267;  Indels   44;  Gaps   17;

Qy      18 GTRIALVVFVGGTLVLGTILFLVSQGLLSLQAKQEYCLKPECIEAAAAILSKVNLSVDPC 77
           |  : |:: :|  : ||       |  |      | : |  | |: ||| ||  :: | :||
Db      19 GLMVLLLLLLGAIVTLGV---FYSIALRDSSLKSDICTTPSCVIAAARILENMDQSRNPC 75

Qy      78 DNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLEKSISRRRDTEAIQKAKI 137
           :||:::|| ||: :: |||    | |:  ||  ::: || :|| | |: |   |::|||
Db      76 ENFYQYACGGWLRHHVIPETNSRYSVFDILRDELEVILKGVLEDSTSQHR--PAVEKAKT 133
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Qy    138 LYSSCMNEKAIEKADAKPLLHILRHSPFRWPVLESNIGPEGVWSER---KFSLLQTLATF 194
          || |||:  ||| |::||| :|:     |||              |:|    |: | : ||
Db    134 LYRSCMNQSVIEKRDSEPLLSVLK-MVGGWPVALDK------WNETMGLKWELERQLAVL 186

Qy    195 RGQYSNSVFIRLYVSPDDKASNEHILKLDQATLSLAVREDYLDNSTEAKSYRDALYKFMV 254
            |::  | | |::  ||: |: |:: :|| || :  || |       |  | |  :||
Db    187 NSQFNRRVLIDLFIWNDDQNSSRHVIYIDQPTLGMPSREYYFQEDNNHK-VRKAYPEFMT 245

Qy    255 DTAVL------LGANSSRAEHDMKSVLRLEIKIAEIMIPHENRTS-EAMYNKMNISELSA 307
            | :      |   |:    :|  || ||  :|   :| | |    |:|::|:: ||
Db    246 SVATMLRKDQNLSKESAMVREEMAEVLELETHLANATVPQEKRHDVTALYHRMDLMELQE 305

Qy    308 M--IPQFDWLGYIKKV---IDTRLYPHLKDISPSENVVVRVPQYFKDLFRILGSERKKTI 362
             :  |:|  :|: |   ::  |:       | | |||    | ::|  |: |   :|:
Db    306 RFGLKGFNWTLFIQNVLSSVEVELF-------PDEEVVVYGIPYLENLEDIIDSYSARTM 358

Qy    363 ANYLVWRMVYSRIPNLSRRFQYRWLEFSRVIQGTTTLLPQWDKCVNFIESALPYVVGKMF 422
          ||||||:|  || :||:||:   ::: : : |||    :| :||::: | :   || ::
Db    359 QNYLVWRLVLDRIGSLSQRFKEARVDYRKALYGTTVEEVRWRECVSYVNSNMESAVGSLY 418

Qy    423 VDVYFQEDKKEMMEELVEGVRWAFIDMLEKENEWMDAGTKRKAKEKARAVLAKVGYPEFI 482
          :   | :| |  : ||:| :|  |:| |:: | |||  :|:||:|||  :  ::|||::|
Db    419 IKRAFSKDSKSTVRELIEKIRSVFVDNLDELN-WMDEESKKKAQEKAMNIREQIGYPDYI 477

Qy    483 M--NDTHVNEDLKAIKFSEADYFGNVLQTRKYLAQSDFFWLRKAVPKTEWFTNPTTVNAF 540
          :  |: |::|:  :: | |  || | ||  |  ||     ||: | :  |       ||||
Db    478 LEDNNKHLDEEYSSLTFYEDLYFENGLQNLKNNAQRSLKKLREKVDQNLWIIGAAVVNAF 537

Qy    541 YSASTNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNGRKYDKNGNLD 600
          || : ||| |||| || |||   : |:||::| ||:::||| |||||:||| :|||||:
Db    538 YSPNRNQIVFPAGILQPPFF-SKDQPQSLNFGGIGMVIGHEITHGFDDNGRNFDKNGNML 596

Qy    601 PWWSTESEEKFKEKTKCMINQYSNYYWKKA-GLNVKGKRTLGENIADNGGLREAFRAYRK 659
           ||| |   |:::::|||  || |: |: |   || |  :|||||||||:|:|:::|| :
Db    597 DWWSNFSARHFQQQSQCMIYQYGNFSWELADNQNVNGFSSLGENIADNGGVRQAYKAYLR 656

Qy    660 WINDRRQGLEEPLLPGITFTNNQLFFLSYAHVRCNSYRPEAAREQVQIGAHSPPQFRVNG 719
          |: |   | ::  |||:  |  ||||::|| | | ||||| | : ::   ||| ::|| |
Db    657 WLAD---GGKDQRLPGLNLTYAQLFFINYAQVWCGSYRPEFAVQSIKTDVHSPLKYRVLG 713

Qy    720 AISNSEEFQKAFNCPPNSTMNRGMDSCRLW 749
          :: |   | :||:||  | |:  |  ||:|
Db    714 SLQNLPGFSEAFHCPRGSPMH-PMKRCRIW 742


RESULT 5
Q9QZV7
ID   Q9QZV7      PRELIMINARY;      PRT;   765 AA.
AC   Q9QZV7;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Soluble secreted endopeptidase.
GN   MELL1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20011457; PubMed=10542292;
RA   Ikeda K., Emoto N., Raharjo S.B., Nurhantari Y., Saiki K.,
RA   Yokoyama M., Matsuo M.;
RT   "Molecular identification and characterization of novel membrane-bound
RT   metalloprotease, the soluble secreted form of which hydrolyzes a
RT   variety of vasoactive peptides.";
RL   J. Biol. Chem. 274:32469-32477(1999).
DR   EMBL; AF157105; AAF13152.1; -.
DR   HSSP; P08473; 1DMT.
DR   MEROPS; M13.008; -.
DR   MGD; MGI:1351603; Mell1.
DR   InterPro; IPR000718; Peptidase_M13.
DR   InterPro; IPR001230; Prenyl_site.
DR   InterPro; IPR000130; Zn_MTpeptdse.
DR   Pfam; PF01431; Peptidase_M13; 1.
DR   PRINTS; PR00786; NEPRILYSIN.
DR   PROSITE; PS00294; PRENYLATION; UNKNOWN_1.
DR   PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
SQ   SEQUENCE   765 AA;  88651 MW;  567D3C17764C0F3F CRC64;

  Query Match             34.6%;  Score 1368.5;  DB 11;  Length 765;
  Best Local Similarity   38.7%;  Pred. No. 2.3e-86;
  Matches  294;  Conservative  148;  Mismatches  267;  Indels   51;  Gaps   18;

Qy     18 GTRIALVVF--VGGTLVLGTILF--------LVSQGLLSLQAKQEYCLKPECIEAAAAIL 67
          |  : | ||  :|  | | | |          :| : |     | : |  | |: ||| ||
Db     29 GAIVTLGVFYSIGKQLPLLTSLLHFSWDERTVVKRALRDSSLKSDICTTPSCVIAAARIL 88

Qy     68 SKVNLSVDPCDNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLEKSISRRR 127
            :: | :||:||:::|| ||: :: |||    | |:  ||  ::: || :|| | |: |
Db     89 ENMDQSRNPCENFYQYACGGWLRHHVIPETNSRYSVFDILRDELEVILKGVLEDSTSQHR 148

Qy    128 DTEAIQKAKILYSSCMNEKAIEKADAKPLLHILRHSPFRWPVLESNIGPEGVWSER---K 184
             |::||| || ||||:  ||| |::||| :|:     |||           |:|    |
Db    149 --PAVEKAKTLYRSCMNQSVIEKRDSEPLLSVLK-MVGGWPVALDK------WNETMGLK 199

Qy    185 FSLLQTLATFRGQYSNSVFIRLYVSPDDKASNEHILKLDQATLSLAVREDYLDNSTEAKS 244
          : | : ||     |::  | | |::  ||: |: |:: :|| || :  || |       |
Db    200 WELERQLAVLNSQFNRRVLIDLFIWNDDQNSSRHVIYIDQPTLGMPSREYYFQEDNNHK- 258

Qy    245 YRDALYKFMVDTAVL------LGANSSRAEHDMKSVLRLEIKIAEIMIPHENRTS-EAMY 297
           | |  :||   | :       |   |:    :|  || ||  :|   :| | |    |:|
Db    259 VRKAYPEFMTSVATMLRKDQNLSKESAMVREEMAEVLELETHLANATVPQEKRHDVTALY 318

Qy    298 NKMNISELSAM--IPQFDWLGYIKKV---IDTRLYPHLKDISPSENVVVRVPQYFKDLFR 352
          ::|:: ||     :  |:|  :|: |   ::  |:       | | |||    | ::|
Db    319 HRMDLMELQERFGLKGFNWTLFIQNVLSSVEVELF-------PDEEVVVYGIPYLENLED 371

Qy    353 ILGSERKKTIANYLVWRMVYSRIPNLSRRFQYRWLEFSRVIQGTTTLLPQWDKCVNFIES 412
          |: |   :|: |||||||:|  || :||:||:   ::: : : |||    :| :||::: |
Db    372 IIDSYSARTMQNYLVWRLVLDRIGSLSQRFKEARVDYRKALYGTTVEEVRWRECVSYVNS 431

Qy    413 ALPYVVGKMFVDVYFQEDKKEMMEELVEGVRWAFIDMLEKENEWMDAGTKRKAKEKARAV 472
           :   || :::   | :| |  : ||:| :|  |:| |:: | |||  :|:||:|||  :
Db    432 NMESAVGSLYIKRAFSKDSKSTVRELIEKIRSVFVDNLDELN-WMDEESKKKAQEKAMNI 490

Qy    473 LAKVGYPEFIM--NDTHVNEDLKAIKFSEADYFGNVLQTRKYLAQSDFFWLRKAVPKTEW 530
            ::|||::|:  |: |::|:  :: | |  || | ||  | ||     ||: | :  |
Db    491 REQIGYPDYILEDNNKHLDEEYSSLTFYEDLYFENGLQNLKNNAQRSLKKLREKVDQNLW 550

Qy    531 FTNPTTVNAFYSASTNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNG 590
                |||||| : ||| |||| || |||   : |:||::| ||:::||| |||||:||
Db    551 IIGAAVVNAFYSPNRNQIVFPAGILQPPFF-SKDQPQSLNFGGIGMVIGHEITHGFDDNG 609

Qy    591 RKYDKNGNLDPWWSTESEEKFKEKTKCMINQYSNYYWKKA-GLNVKGKRTLGENIADNGG 649
          | :|||||:  |||  |   |:::::||| || |: |: |   || |  :||||||||||
Db    610 RNFDKNGNMLDWWSNFSARHFQQQSQCMIYQYGNFSWELADNQNVNGFSSLGENIADNGG 669

Qy    650 LREAFRAYRKWINDRRQGLEEPLLPGITFTNNQLFFLSYAHVRCNSYRPEAAREQVQIGA 709
          :|:|::|| :|: |   | ::  |||:  |  ||||::|| | | ||||| | : ::
Db    670 VRQAYKAYLRWLAD---GGKDQRLPGLNLTYAQLFFINYAQVWCGSYRPEFAVQSIKTDV 726

Qy    710 HSPPQFRVNGAISNSEEFQKAFNCPPNSTMNRGMDSCRLW 749
          |||  ::|| |:: |   | :||:||  | |:  |  ||:|
Db    727 HSPLKYRVLGSLQNLPGFSEAFHCPRGSPMH-PMKRCRIW 765


RESULT 6
Q9ERK2
ID   Q9ERK2      PRELIMINARY;      PRT;   779 AA.
AC   Q9ERK2;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Neprilysin-like peptidase gamma.
```

```
GN   MELL1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21293028; PubMed=11278416;
RA   Shirotani K., Tsubuki S., Iwata N., Takaki Y., Harigaya W.,
RA   Maruyama K., Kiryu-Seo S., Kiyama H., Iwata H., Tomita T.,
RA   Iwatsubo T., Saido T.C.;
RT   "Neprilysin Degrades Both Amyloid beta Peptides 1-40 and 1-42 Most
RT   Rapidly and Efficiently among Thiorphan- and Phosphoramidon-sensitive
RT   Endopeptidases.";
RL   J. Biol. Chem. 276:21895-21901(2001).
DR   EMBL; AF302077; AAG18448.1; -.
DR   HSSP; P08473; 1DMT.
DR   MEROPS; M13.008; -.
DR   MGD; MGI:1351603; Mell1.
DR   InterPro; IPR000718; Peptidase_M13.
DR   InterPro; IPR001230; Prenyl_site.
DR   InterPro; IPR000130; Zn_MTpeptdse.
DR   Pfam; PF01431; Peptidase_M13; 1.
DR   PRINTS; PR00786; NEPRILYSIN.
DR   PROSITE; PS00294; PRENYLATION; UNKNOWN_1.
DR   PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
SQ   SEQUENCE   779 AA;  89709 MW;  5E48CA530828584B CRC64;

  Query Match             34.4%;  Score 1361.5;  DB 11;  Length 779;
  Best Local Similarity   37.0%;  Pred. No. 7.3e-86;
  Matches  291;  Conservative  148;  Mismatches  267;  Indels   81;  Gaps   17;

Qy      18 GTRIALVVFVGGTLVLGTILFLVSQGLLSLQAKQEYCLKPECIEAAAAILSKVNLSVDPC 77
           |  : |:: :|  : ||      |  |      | : |  | |: ||| ||  :: | :||
Db      19 GLMVLLLLLLGAIVTLGV---FYSIALRDSSLKSDICTTPSCVIAAARILENMDQSRNPC 75

Qy      78 DNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLEKSISRRRDTEAIQKAKI 137
           :||:::|| ||: :: |||    | |:  ||  ::: || :|| | |: |   |::|||
Db      76 ENFYQYACGGWLRHHVIPETNSRYSVFDILRDELEVILKGVLEDSTSQHR--PAVEKAKT 133

Qy     138 LYSSCMNEKAIEKADAKPLLHILRHSPFRWPVLESNIGPEGVWSER---KFSLLQTLATF 194
           || ||||:  ||| |::||| :|:     |||          |:|     |: | : ||
Db     134 LYRSCMNQSVIEKRDSEPLLSVLK-MVGGWPVAMDK------WNETMGLKWELERQLAVL 186

Qy     195 RGQYSNSVFIRLYVSPDDKASNEHILKLDQATLSLAVREDYLDNSTEAKSYRDALYKFMV 254
             |::  | | |::  ||: |: |: |:: :|| || :  || |       |  | |  :||
Db     187 NSQFNRRVLIDLFIWNDDQNSSRHVIYIDQPTLGMPSREYYFQEDNNHK-VRKAYLEFMT 245

Qy     255 DTAVL------LGANSSRAEHDMKSVLRLEIKIAEIMIPHENRTS-EAMYNKMNISELSA 307
             | :      |   |:     :|  || ||  :|   :| | |     |:|::|:: ||
Db     246 SVATMLRKDQNLSKESAMVREEMAEVLELETHLANATVPQEKRHDVTALYHRMDLMELQE 305

Qy     308 M-----------------------------------IPQFDWLGYIKKV---IDTR 325
                                                 :  |:|  :|: |   ::
Db     306 RFGLKDRVSLCSPGCPGTHSVDQAGLELGNPPASDSRVLGLKGFNWTLFIQNVLSSVEVE 365

Qy     326 LYPHLKDISPSENVVVRVPQYFKDLFRILGSERKKTIANYLVWRMVYSRIPNLSRRFQYR 385
           |:       | | |||    | ::|  |: |   :|: |||||:|  || :||:||:
Db     366 LF-------PDEEVVVYGIPYLENLEDIIDSYSARTMQNYLVWRLVLDRIGSLSQRFKEA 418

Qy     386 WLEFSRVIQGTTTLLPQWDKCVNFIESALPYVVGKMFVDVYFQEDKKEMMEELVEGVRWA 445
             ::: : :|||    :| :||::: | :   || :::   | :| |  : ||:| :|
Db     419 RVDYRKALYGTTVEEVRWRECVSYVNSNMESAVGSLYIKRAFSKDSKSTVRELIEKIRSV 478

Qy     446 FIDMLEKENEWMDAGTKRKAKEKARAVLAKVGYPEFIM--NDTHVNEDLKAIKFSEADYF 503
           |:| |:: | |||  :|:||:|||  :  ::|||::|:  |: |::|:  :: | |  ||
Db     479 FVDNLDELN-WMDEESKKKAQEKAMNIREQIGYPDYILEDNNKHLDEEYSSLTFYEDLYF 537

Qy     504 GNVLQTRKYLAQSDFFWLRKAVPKTEWEFTNPTTVNAFYSASTNQIRFPAGELQKPFFWGT 563
             | ||  |  ||     ||: | :  |      |||||| : ||| |||| || |||
Db     538 ENGLQNLKNNAQRSLKKLREKVDQNLWIIGAAVVNAFYSPNRNQIVFPAGILQPPFF-SK 596

Qy     564 EYPRSLSYGAIGVIVGHEFTHGFDNNGRKYDKNGNLDPWWSTESEEKFKEKTKCMINQYS 623
```

```
           : |:||::| ||:::||| |||||:||| :||||||:  |||  |   |:::::||| ||
Db     597 DQPQSLNFGGIGMVIGHEITHGFDDNGRNFDKNGNMLDWWSNFSARHFQQQSQCMIYQYG 656

Qy     624 NYYWKKA-GLNVKGKRTLGENIADNGGLREAFRAYRKWINDRRQGLEEPLLPGITFTNNQ 682
           |: |: |   || |  |||||||||||:|:|::|| :|: |   | ::  |||:  |  |
Db     657 NFSWELADNQNVNGFSTLGENIADNGGVRQAYKAYLRWLAD---GGKDQRLPGLNLTYAQ 713

Qy     683 LFFLSYAHVRCNSYRPEAAREQVQIGAHSPPQFRVNGAISNSEEFQKAFNCPPNSTMNRG 742
           |||::|| | | ||||| | : ::   ||| ::|| |:: |   | :||:||  | |:
Db     714 LFFINYAQVWCGSYRPEFAVQSIKTDVHSPLKYRVLGSLQNLPGFSEAFHCPRGSPMH-P 772

Qy     743 MDSCRLW 749
           |  ||:|
Db     773 MKRCRIW 779


RESULT 7
O93394
ID   O93394      PRELIMINARY;      PRT;   770 AA.
AC   O93394;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Neprilysin.
GN   NEP1.
OS   Perca flavescens (Yellow perch).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidei;
OC   Percidae; Perca.
OX   NCBI_TaxID=8167;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=OVULATORY OVARY;
RX   MEDLINE=99445407; PubMed=10514552;
RA   Langenau D.M., Goetz F.W., Roberts S.B.;
RT   "The upregulation of messenger ribonucleic acids during 17alpha,
RT   20beta-dihydroxy-4-pregnen-3-one-induced ovulation in the perch
RT   ovary.";
RL   J. Mol. Endocrinol. 23:137-152(1999).
DR   EMBL; AF077612; AAC28366.1; -.
DR   HSSP; P08473; 1DMT.
DR   MEROPS; M13.001; -.
DR   InterPro; IPR000718; Peptidase_M13.
DR   InterPro; IPR001230; Prenyl_site.
DR   InterPro; IPR000130; Zn_MTpeptdse.
DR   Pfam; PF01431; Peptidase_M13; 1.
DR   PRINTS; PR00786; NEPRILYSIN.
DR   PROSITE; PS00294; PRENYLATION; UNKNOWN_1.
DR   PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
SQ   SEQUENCE   770 AA;  88135 MW;  D29F216CB041BACC CRC64;

  Query Match             33.7%;  Score 1335;  DB 13;  Length 770;
  Best Local Similarity   38.0%;  Pred. No. 5e-84;
  Matches  294;  Conservative  146;  Mismatches  283;  Indels   50;  Gaps   21;

Qy       3 AETGS--SVETG--KKANRGTRIALVVFVGGTLVLGTILFLVSQGLLSLQAKQ---EYCL 55
           || |    :||   | | :    :| |   |   : ::|| :|   |: | | |   | |
Db      22 AEAGDLRMMETNPPKSAKKPRWTSLEV---GLTTIVSLLFIVIVALIILFATQKTDEICT 78

Qy      56 KPECIEAAAAILSKVNLSVDPCDNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKL 115
             :| ::|: ::  :: |||||||||:::|| ||:  | |||    |  :  ||  ::: |
Db      79 TGDCTQSASRLIENMDDSVDPCDNFYQYACGGWLKKNIIPETSSRYSTFDILRDELEVIL 138

Qy     116 KELLEKSISRRRDTEAIQKAKILYSSCMNEKAIEKADAKPLLHILRHSPFRWPVL----E 171
           | :|||  :   :     :|| || || ||  ||     ||| :|    | |||     |
Db     139 KGVLEK--TDEGEATLSTRAKTLYKSCTNESLIELRGGAPLLDML-PDVFEWPVAVDNWE 195

Qy     172 SNIGPEGVWSERKFSLLQTLATFRGQYSNSVFIRLYVSPDDKASNEHILKLDQAT-LSLA 230
           :| |       : : |   :|   :|   :  :  :| ||: || :|:  || | | |
Db     196 TNYG-------KTWRLEDVIAKLNEKYGTQLLVNFFVGTDDRDSNSYIIHFDQQTNLGLL 248

Qy     231 VREDYLDNSTEAKSYRDALYKFMVDTAVLL----GANSSRAE--HDMKSVLRLEIKIAEI 284
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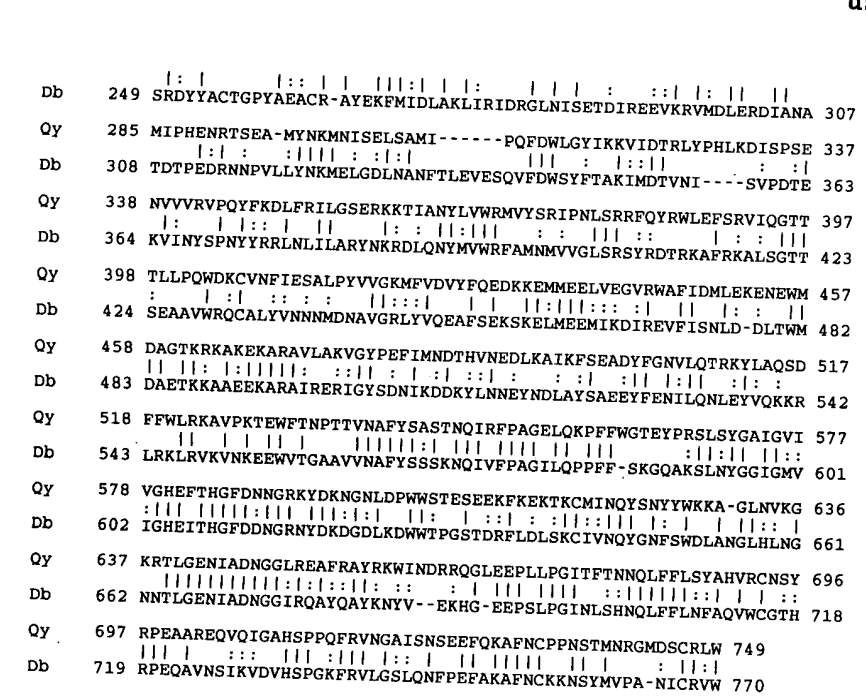

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Db    249 SRDYYACTGPYAEACR-AYEKFMIDLAKLIRIDRGLNISETDIREEVKRVMDLERDIANA 307

Qy    285 MIPHENRTSEA-MYNKMNISELSAMI------PQFDWLGYIKKVIDTRLYPHLKDISPSE 337

Db    308 TDTPEDRNNPVLLYNKMELGDLNANFTLEVESQVFDWSYFTAKIMDTVNI----SVPDTE 363

Qy    338 NVVVRVPQYFKDLFRILGSERKKTIANYLVWRMVYSRIPNLSRRFQYRWLEFSRVIQGTT 397

Db    364 KVINYSPNYYRRLNLILARYNKRDLQNYMVWRFAMNMVVGLSRSYRDTRKAFRKALSGTT 423

Qy    398 TLLPQWDKCVNFIESALPYVVGKMFVDVYFQEDKKEMMEELVEGVRWAFIDMLEKENEWM 457

Db    424 SEAAVWRQCALYVNNNMDNAVGRLYVQEAFSEKSKELMEEMIKDIREVFISNLD-DLTWM 482

Qy    458 DAGTKRKAKEKARAVLAKVGYPEFIMNDTHVNEDLKAIKFSEADYFGNVLQTRKYLAQSD 517

Db    483 DAETKKAAEEKARAIRERIGYSDNIKDDKYLNNEYNDLAYSAEEYFENILQNLEYVQKKR 542

Qy    518 FFWLRKAVPKTEWFTNPTTVNAFYSASTNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVI 577

Db    543 LRKLRVKVNKEEWVTGAAVVNAFYSSSKNQIVFPAGILQPPFF-SKGQAKSLNYGGIGMV 601

Qy    578 VGHEFTHGFDNNGRKYDKNGNLDPWWSTESEEKFKEKTKCMINQYSNYYWKKA-GLNVKG 636

Db    602 IGHEITHGFDDNGRNYDKDGDLKDWWTPGSTDRFLDLSKCIVNQYGNFSWDLANGLHLNG 661

Qy    637 KRTLGENIADNGGLREAFRAYRKWINDRRQGLEEPLLPGITFTNNQLFFLSYAHVRCNSY 696

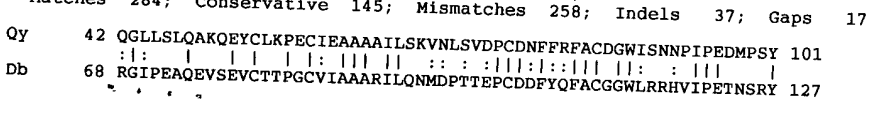
Db    662 NNTLGENIADNGGIRQAYQAYKNYV--EKHG-EEPSLPGINLSHNQLFFLNFAQVWCGTH 718

Qy    697 RPEAAREQVQIGAHSPPQFRVNGAISNSEEFQKAFNCPPNSTMNRGMDSCRLW 749

Db    719 RPEQAVNSIKVDVHSPGKFRVLGSLQNFPEFAKAFNCKKNSYMVPA-NICRVW 770
```

RESULT 8
Q96PH9
ID Q96PH9 PRELIMINARY; PRT; 770 AA.
AC Q96PH9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Neprilysin-like metallopeptidase 2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21444797; PubMed=11560781;
RA Bonvouloir N., Lemieux N., Crine P., Boileau G., DesGroseillers L.;
RT "Molecular cloning, tissue distribution, and chromosomal localization
RT of MMEL2, a gene coding for a novel human member of the neutral
RT endopeptidase-24.11 family.";
RL DNA Cell Biol. 20:493-498(2001).
DR EMBL; AF336981; AAL08942.1; -.
DR MEROPS; M13.008; -.
DR InterPro; IPR000718; Peptidase_M13.
DR InterPro; IPR001230; Prenyl_site.
DR InterPro; IPR000130; Zn_MTpeptdse.
DR Pfam; PF01431; Peptidase_M13; 1.
DR PROSITE; PS00294; PRENYLATION; UNKNOWN_1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
SQ SEQUENCE 770 AA; 88523 MW; DF9C08F4AA56A23B CRC64;

Query Match 33.7%; Score 1332.5; DB 4; Length 770;
Best Local Similarity 39.2%; Pred. No. 7.4e-84;
Matches 284; Conservative 145; Mismatches 258; Indels 37; Gaps 17;



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Qy     42 QGLLSLQAKQEYCLKPECIEAAAAILSKVNLSVDPCDNFFRFACDGWISNNPIPEDMPSY 101

Db     68 RGIPEAQEVSEVCTTPGCVIAAARILQNMDPTTEPCDDFYQFACGGWLRRHVIPETNSRY 127
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Qy    102 GVYPWLRHNVDLKLKELLEKSISRRRDTEAIQKAKILYSSCMNEKAIEKADAKPLLHILR 161

Db    128 SIFDVLRDELEVILKAVLENSTA--KDRPAVEKARTLYRSCMNQSVIEKRGSQPLLDIL- 184

Qy    162 HSPFRWPVLESNIGPEGVWSER---KFSLLQTLATFRGQYSNSVFIRLYVSPDDKASNEH 218

Db    185 EVVGGWPVAMDR------WNETVGLEWELERQLALMNSQFNRRVLIDLFIWNDDQNSSRH 238

Qy    219 ILKLDQATLSLAVREDYLDNSTEAKSYRDALYKFMVDTAVLL--GANSSR----AEHDMK 272

Db    239 IIYIDQPTLGMPSREYYFNGGSNRK-VREAYLQFMVSVATLLREDANLPRDSCLVQEDMV 297

Qy    273 SVLRLEIKIAEIMIPHENRTSE-AMYNKMNISELSAM--IPQFDWLGYIKKVIDTRLYPH 329

Db    298 QVLELETQLAKATVPQEERHDVIALYHRMGLEELQSQFGLKGFNWTLFIQTVLSS----- 352

Qy    330 LK-DISPSENVVVRVPQYFKDLFRILGSERKKTIANYLVWRMVYSRIPNLSRRFQYRWLE 388

Db    353 VKIKLLPDEEVVVYGIPYLQNLENIIDTYSARTIQNYLVWRLVLDRIGSLSQRFKDTRVN 412

Qy    389 FSRVIQGTTTLLPQWDKCVNFIESALPYVVGKMFVDVYFQEDKKEMMEELVEGVRWAFID 448

Db    413 YRKALFGTMVEEVRWRECVGYVNSNMENAVGSLYVREAFPGDSKSMVRELIDKVRTVFVE 472

Qy    449 MLEKENEWMDAGTKRKAKEKARAVLAKVGYPEFIMNDTH--VNEDLKAIKFSEADYFGNV 506

Db    473 TLD-ELGWMDEESKKKAQEKAMSIREQIGHPDYILEEMNRRLDEEYSNLNFSEDLYFENS 531

Qy    507 LQTRKYLAQSDFFWLRKAVPKTEWFTNPTTVNAFYSASTNQIRFPAGELQKPFFWGTEYP 566

Db    532 LQNLKVGAQRSLRKLREKVDPNLWIIGAAVVNAFYSPNRNQIVFPAGILQPPFF-SKEQP 590

Qy    567 RSLSYGAIGVIVGHEFTHGFDNNGRKYDKNGNLDPWWSTESEEKFKEKTKCMINQYSNYY 626

Db    591 QALNFGGIGMVIGHEITHGFDDNGRNFDKNGNMMDWWSNFSTQHFREQSECMIYQYGNYS 650

Qy    627 WKKAG-LNVKGKRTLGENIADNGGLREAFRAYRKWINDRRQGLEEPLLPGITFTNNQLFF 685

Db    651 WDLADEQNVNGFNTLGENIADNGGVRQAYKAYLKWM---AEGGKDQQLPGLDLTHEQLFF 707

Qy    686 LSYAHVRCNSYRPEAAREQVQIGAHSPPQFRVNGAISNSEEFQKAFNCPPNSTMNRGMDS 745

Db    708 INYAQVWCGSYRPEFAIQSIKTDVHSPLKYRVLGSLQNLAAFADTFHCARGTPMH-PKER 766

Qy    746 CRLW 749

Db    767 CRVW 770
```

RESULT 9
Q9DGN6
ID Q9DGN6 PRELIMINARY; PRT; 752 AA.
AC Q9DGN6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Endothelin converting enzyme-1.
GN ECE-1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20363660; PubMed=10903177;
RA Takebayashi-Suzuki K., Yanagisawa M., Gourdie R.G., Kanzawa N.,
RA Mikawa T.;
RT "In vivo induction of cardiac Purkinje fiber differentiation by
RT coexpression of preproendothelin-1 and endothelin converting enzyme-
RT 1.";
RL Development 127:3523-3532(2000).

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DR   EMBL; AF230274; AAF98287.1; -.
DR   HSSP; P08473; 1DMT.
DR   MEROPS; M13.002; -.
DR   InterPro; IPR000718; Peptidase_M13.
DR   InterPro; IPR000130; Zn_MTpeptdse.
DR   Pfam; PF01431; Peptidase_M13; 1.
DR   PRINTS; PR00786; NEPRILYSIN.
DR   PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
SQ   SEQUENCE   752 AA;  84985 MW;  3B6B3DB7BF900656 CRC64;

  Query Match           31.8%;  Score 1257;  DB 13;  Length 752;
  Best Local Similarity   37.5%;  Pred. No. 1.2e-78;
  Matches  278;  Conservative  138;  Mismatches  271;  Indels   54;  Gaps   20;

Qy      21 IALVVFVGGTLVLGTILFLVSQGLLSLQAK-QEYCLKPECIEAAAAILSKVNLSVDPCDN 79
           :|::  | |  :|| :         |  :|:    ||   ||   ::||| :: :|:||::
Db      54 VAVLAAVLGACLLGLV--------LQYRARPPAVCLSEACISVTSSILSSLDRTVNPCED 105

Qy      80 FFRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLEKSISRRRDTEAIQKAKILY 139
           || :|| ||:  ||:|:    :| :  |  :     :| ||| : :    :|| :||:  |
Db     106 FFSYACGGWVKANPLPDGHSRWGTFNNLWEHNQAVMKHLLENT-TANVSSEAERKAQRYY 164

Qy     140 SSCMNEKAIEKADAKPLLHILRHSPFRWPVLESNIGP---EGVWSERKFSLLQTLATFRG 196
           :|||| ||:  | ||: ::          : :|     | |:   |:   ||
Db     165 QACMNESKIEELRAAPLMELI----------AKLGGWNITGPWAGGDFN--ATLREVTA 211

Qy     197 QYSNSVFIRLYVSPDDKASNEHILKLDQATLSLAVREDYLDNSTEAKSYRDALYKFMVDT 256
           |  | |  :||| | | || :::::||: | |  |: || | || :         :||
Db     212 HYRISPFFSVYVSADSKNSNSNVIQVDQSGLGLPSRDYYL-NKTENEKVLAGYLNYMVQL 270

Qy     257 AVLLGANSSRA-EHDMKSVLRLEIKIAEIMIPHE-NRTSEAMYNKMNISELSAMIPQFDW 314
           : ||     :   |: :|  |  :| | || | :|  | :|:||   ||  : |  ||
Db     271 GMFLGGTDEESTRQQMQQILEFETALANITIPQEKHRDEEVIYHKMTAGELKDLAPAVDW 330

Qy     315 LGYIKKVIDTRLYPHLKDISPSENVVVRVPQYFKDLFRILGSERKKTIANYLVWRMVYSR 374
           : ::  |     ||   ::: || |||   :| : :  :: :  |  : ||::| :|
Db     331 MPFLSTV----FYP--VELNESEPVVVYAKEYLEQVSDLILATDKCLLNNYMIWNLVRKT 384

Qy     375 IPNLSRRFQYRWLEFSRVIQGT-TTLLPQWDKCVNFIESALPYVVGKMFVDVYFQEDKKE 433
           | | :|||    :|  |: ||  | ||:|  |::  :: | : :| |||   | || |:
Db     385 SPFLDQRFQDAEEKFMEVMYGTKKTCLPRWKFCISDTDNNLGFALGAMFVKATFAEDSKQ 444

Qy     434 MMEELVEGVRWAFIDMLEKENEWMDAGTKRKAKEKARAVLAKVGYPEFIMNDTHVNEDLK 493
           : ||::  :: || : ||  :|||  |:: ||||| |:   :|||:||::   :::
Db     445 VAEEMIAEIKTAFEESLE-TLQWMDEETRKSAKEKADAIYNMIGYPKFILDSKELDK--- 500

Qy     494 AIKFSEAD-----YFGNVLQTRKYLAQSDFFWLRKAVPKTEWFTNPTTVNAFYSASTNQI 548
           |:: |      || ||:|   : |:     |||   : :|   | ||||:|| : |:|
Db     501 --VFNDYDAVSDLYFENVMQFYNFSARVTADQLRKPPNRDQWSMTPPTVNAYYSPTKNEI 558

Qy     549 RFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNGRKYDKNGNLDPWWSTESE 608
           |||| || ||:     |:||::| |||:|||| || ||: ||:|||:||| |||    |
Db     559 VFPAGILQAPFYTRAS-PKSLNFGGIGVVVGHELTHAFDDQGREYDKDGNLRPWWKNSSV 617

Qy     609 EKFKEKTKCMINQYSNYYWKKAGLNVKGKRTLGENIADNGGLREAFRAYRKWINDRRQGL 668
           | || :| ||: |||||     |  | || ||||||||||||: |:|||: |:  |: |
Db     618 EAFKRQTACMVEQYSNYTIN--GEAVNGKHTLGENIADNGGLKAAYRAYQNWL--RKNG- 672

Qy     669 EEPLLPGITFTNNQLFFLSYAHVRCNSYRPEAAREQVQIGAHSPPQFRVNGAISNSEEFQ 728
           ||  || :  ||:||||: :| | |:   ||:: | :    ||| :||| | :||| ||
Db     673 EEETLPTLGLTNHQLFFVGFAQVWCSVRTPESSHEGLITDPHSPSRFRVIGTVSNSWEFA 732

Qy     729 KAFNCPPNSTMNRGMDSCRLW 749
           : |:||  | ||     | :|
Db     733 EHFSCPLGSPMN-PPKKCEVW 752


RESULT 10
Q28868
ID   Q28868      PRELIMINARY;      PRT;   758 AA.
AC   Q28868;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Endothelin converting enzyme.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95032010; PubMed=7945289;
RA   Ikura T., Sawamura T., Shiraki T., Hosokawa H., Kido T., Hoshikawa H.,
RA   Shimada K., Tanzawa K., Kobayashi S., Miwa S., et al;
RT   "cDNA cloning and expression of bovine endothelin converting enzyme.";
RL   Biochem. Biophys. Res. Commun. 203:1417-1422(1994).
DR   EMBL; S73774; AAB32062.1; -.
DR   HSSP; P08473; 1DMT.
DR   InterPro; IPR000718; Peptidase_M13.
DR   InterPro; IPR000130; Zn_MTpeptdse.
DR   Pfam; PF01431; Peptidase_M13; 1.
DR   PRINTS; PR00786; NEPRILYSIN.
DR   PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
SQ   SEQUENCE   758 AA;  85648 MW;  6A7EA96566BEFEC5 CRC64;

  Query Match           31.7%;  Score 1253.5;  DB 6;  Length 758;
  Best Local Similarity   38.0%;  Pred. No. 2.2e-78;
  Matches  283;  Conservative  121;  Mismatches  280;  Indels   61;  Gaps   21;

Qy      23 LVVFVGGTLVLGTILFLVSQGLLSLQAKQEYCLKPECIEAAAAILSKVNLSVDPCDNFFR 82
           ||| |   |    :  |   |:          ||   ||   ::||| :: :|||| :||
Db      57 LVVLV-ALLAAALVACLAVLGIQYQTRTPSVCLSEACISVTSSILSSMDPTVDPCQDFFT 115

Qy      83 FACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLEKSISRRRDTEAIQKAKILYSSC 142
           :|| |||  ||:|:    :| :  |  :     :| ||| | :    :|| :||:: | :|
Db     116 YACGGWIKANPVPDGHSRWGTFSNLWEHNQAIIKHLLENSTA--SVSEAERKAQVYYRAC 173

Qy     143 MNEKAIEKADAKPLLHILRHSPFRWPVLESNIGPEGVWSERKFSLLQTLATFRGQYSNSV 202
           |||  ||:  ||||: ::          | :         | |  :    ||       | |
Db     174 MNETRIEELKAKPLMELIEKLG-GWNI-------TGPWDKDNFQ--DTLQVVTSHYHTSP 223

Qy     203 FIRLYVSPDDKASNEHILKLDQATLSLAVREDYLDNSTEAKSYRDALYKFMVDTAVLLGA 262
           |  :||| | | || :::::||: | |  |: || | || :         :||     |||
Db     224 FFSVYVSADSKNSNSNVIQVDQSGLGLPSRDYYL-NKTENEKVLTGYLNYMVQLGKLLGG 282

Qy     263 NS-SRAEHDMKSVLRLEIKIAEIMIPHENRTSEAM-YNKMNISELSAMIPQFDWLGYIKK 320
           :       |: :|  |  :| | || | :  | :|:|:  :||  : |  :|| :
Db     283 GAEDTIRPQMQQILDFETALANITIPQEKRRDEELIYHKVTAAELQTLAPAINWLPF--- 339

Qy     321 VIDTRLYPHLKDISPSENVVVRVPQYFKDLFRILGSERKKTIANYLVWRMVYSRIPNLSR 380
           ::|  ||   :|: || :|:   :|   :  :: |  |  : ||::| :|      | :
Db     340 -LNTIFYP--VEINESEPIVIYDKEYLSKVSTLINSTDKCLLNNYMIWNLVRKTSSFLDQ 396

Qy     381 RFQYRWLEFSRVIQGT-TTLLPQWDKCVNFIESALPYVVGKMFVDVYFQEDKKEMMEELV 439
           |||   :|  | || | :| ||  ||:|  ||:  |: | : :| |||   | || | :  |::
Db     397 RFQDADEKFMEVMYGTKKTCLPRWKFCVSDTENTLGFALGPMFVKATFAEDSKNIASEII 456

Qy     440 EGVRWAFIDMLEKENEWMDAGTKRKAKEKARAVLAKVGYPEFIM---------NDTHVNE 490
           :: || : |    :|||  |:: ||||| |:   :||| |||          ||
Db     457 LEIKKAFEESL-STLKWMDEDTRKSAKEKADAIYNMIGYPNFIMDPKELDKVFNDYTAVP 515

Qy     491 DLKAIKFSEADYFGNVLQTRKYLAQSDFFW------LRKAVPKTEWFTNPTTVNAFYSAS 544
           ||          || | ::          :| |      ||||  : :|   |  |||:|| :
Db     516 DL---------YFENAMRF------FNFSWRVTADQLRKAPNRDQWSMTPPMVNAYYSPT 560

Qy     545 TNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNGRKYDKNGNLDPWWS 604
           |:| |||| || ||:  :  | :|::| |||:|||| || ||: ||:|||:||| |||
Db     561 KNEIVFPAGILQAPFYTRSS-PNALNFGGIGVVVGHELTHAFDDQGREYDKDGNLRPWWK 619

Qy     605 TESEEKFKEKTKCMINQYSNYYWKKAGLNVKGKRTLGENIADNGGLREAFRAYRKWINDR 664
           | | ||::| ||: || ||     |  | |: ||||||||||||: |:|||: |:  :
Db     620 NSSVEAFKQQTACMVEQYGNY--SVNGEPVNGRHTLGENIADNGGLKAAYRAYQNWV--K 675

Qy     665 RQGLEEPLLPGITFTNNQLFFLSYAHVRCNSYRPEAAREQVQIGAHSPPQFRVNGAISNS 724
           : | |:  || :  ||||||||||:| | |:   ||:: | :    ||| :||| |:||||
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Db    676 KNGAEQ-TLPTLGLTNNQLFFLSFAQVWCSVRTPESSHEGLITDPHSPSRFRVIGSISNS 734

Qy    725 EEFQKAFNCPPNSTMNRGMDSCRLW 749
          :|| : |:||| | ||     | :|
Db    735 KEFSEHFHCPPGSPMN-PHHKCEVW 758


RESULT 11
Q28010
ID   Q28010      PRELIMINARY;      PRT;   758 AA.
AC   Q28010;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Endothelin converting enzyme-1a.
GN   ECE-1A.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=94340737; PubMed=8062389;
RA   Xu D., Emoto N., Giaid A., Slaughter C., Kaw S., deWit D.,
RA   Yanagisawa M.;
RT   "ECE-1: a membrane-bound metalloprotease that catalyzes the
RT   proteolytic activation of big endothelin-1.";
RL   Cell 78:473-485(1994).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Yanagisawa M.;
RL   Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U27342; AAA82928.1; -.
DR   HSSP; P08473; 1DMT.
DR   MEROPS; M13.002; -.
DR   InterPro; IPR000718; Peptidase_M13.
DR   InterPro; IPR000130; Zn_MTpeptdse.
DR   Pfam; PF01431; Peptidase_M13; 1.
DR   PRINTS; PR00786; NEPRILYSIN.
DR   PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
SQ   SEQUENCE   758 AA;  85620 MW;  39DCB702099F40A4 CRC64;

  Query Match             31.5%;  Score 1248.5;  DB 6;  Length 758;
  Best Local Similarity   37.9%;  Pred. No. 4.8e-78;
  Matches  282;  Conservative  121;  Mismatches  281;  Indels   61;  Gaps   21;

Qy     23 LVVFVGGTLVLGTILFLVSQGLLSLQAKQEYCLKPECIEAAAAILSKVNLSVDPCDNFFR 82
          ||| |   |    : |   |:              ||   ||   ::||| :: :|||| :||
Db     57 LVVLV-ALLAAALVACLAVLGIQYQTRTPSVCLSEGCISVTSSILSSMDPTVDPCQDFFT 115

Qy     83 FACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLEKSISRRRDTEAIQKAKILYSSC 142
          :|| |||  ||:|:   :| :  |  :    :| ||| | :    :|| :||:: | :|
Db    116 YACGGWIKANPVPDGHSRWGTFSNLWEHNQAIIKHLLENSTA--SVSEAERKAQVYYRAC 173

Qy    143 MNEKAIEKADAKPLLHILRHSPFRWPVLESNIGPEGVWSERKFSLLQTLATFRGQYSNSV 202
          |||  ||:  |||| ::      | :       | | :  |    ||      |  |
Db    174 MNETRIEELKAKPLMELIEKLG-GWNI-------TGPWDKDNFQ--DTLQVVTSHYHTSP 223

Qy    203 FIRLYVSPDDKASNEHILKLDQATLSLAVREDYLDNSTEAKSYRDALYKFMVDTAVLLGA 262
          |  :||| | | || :::::||: | |  |: || | || :          :||   |||
Db    224 FFSVYVSADSKNSNSNVIQVDQSGLGLPSRDYYL-NKTENEKVLTGYLNYMVQLGKLLGG 282

Qy    263 NS-SRAEHDMKSVLRLEIKIAEIMIPHENRTSEAM-YNKMNISELSAMIPQFDWLGYIKK 320
          :      |: :|  |  :| | || | |  | : |:|:  :||  : |  :|| :
Db    283 GAEDTIRPQMQQILDFETALANITIPQEKRRDEELIYHKVTAAELQTLAPAINWLPF--- 339

Qy    321 VIDTRLYPHLKDISPSENVVVRVPQYFKDLFRILGSERKKTIANYLVWRMVYSRIPNLSR 380
          ::|  ||   :|: || :|:   :|   :  :: |  |  : ||::| :|      | :
Db    340 -LNTIFYP--VEINESEPIVIYIDKEYLSKVSTLINSTDKCLLNNYMIWNLVRKTSSFLDQ 396

Qy    381 RFQYRWLEFSRVIQGT-TTLLPQWDKCVNFIESALPYVVGKMFVDVYFQEDKKEMMEELV 439
          |||    :|  |: ||  | ||:|  ||:  |: | : :| |||   | || | :  |::
Db    397 RFQDADEKFMEVMYGTKKTCLPRWKFCVSDTENTLGFALGPMFVKATFAEDSKNIASEII 456

Qy    440 EGVRWAFIDMLEKENEWMDAGTKRKAKEKARAVLAKVGYPEFIM---------NDTHVNE 490
          ::  || : |    :|||  |:: ||||| |:   :||| |||          ||
Db    457 LEIKKAFEESL-STLKWMDEDTRKSAKEKADAIYNMIGYPNFIMDPKELDKVFNDYTAVP 515

Qy    491 DLKAIKFSEADYFGNVLQTRKYLAQSDFFW------LRKAVPKTEWFTNPTTVNAFYSAS 544
          ||          || | ::       :| |      ||||  : :|   |  |||:|| :
Db    516 DL---------YFENAMRF------FNFSWRVTADQLRKAPNRDQWSMTPPMVNAYYSPT 560

Qy    545 TNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNGRKYDKNGNLDPWWS 604
          |:| |||| || ||:  :  | :|:::| |||:|||| || ||: ||:|||:||| |||
Db    561 KNEIVFPAGILQAPFYTRSS-PNALNFGGIGVVVGHELTHAFDDQGREYDKDGNLRPWWK 619

Qy    605 TESEEKFKEKTKCMINQYSNYYWKKAGLNVKGKRTLGENIADNGGLREAFRAYRKWINDR 664
            | | ||::| ||: || ||      |  | |: |||||||||||: |:|||: |:  :
Db    620 NSSVEAFKQQTACMVEQYGNY--SVNGEPVNGRHTLGENIADNGGLKAAYRAYQNWV--K 675

Qy    665 RQGLEEPLLPGITFTNNQLFFLSYAHVRCNSYRPEAAREQVQIGAHSPPQFRVNGAISNS 724
          : | |:  || :  |||||||||:  | |:   ||:: | :    ||| :||| |:||||
Db    676 KNGAEQ-TLPTLGLTNNQLFFLSFGQVWCSVRTPESSHEGLITDPHSPSRFRVIGSISNS 734

Qy    725 EEFQKAFNCPPNSTMNRGMDSCRLW 749
          :|| : |:||| | ||     | :|
Db    735 KEFSEHFHCPPGSPMN-PHHKCEVW 758


RESULT 12
Q9UA44
ID   Q9UA44      PRELIMINARY;      PRT;   787 AA.
AC   Q9UA44;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Neutral endopeptidase.
GN   NEP.
OS   Aplysia californica (California sea hare).
OC   Eukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anaspidea;
OC   Aplysiidae; Aplysia.
OX   NCBI_TaxID=6500;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99274733; PubMed=10341232;
RA   Zappulla J.P., Wickham L., Bawab W., Yang X.F., Storozhuk M.V.,
RA   Castellucci V.F., DesGroseillers L.;
RT   "Cloning and characterization of Aplysia neutral endopeptidase, a
RT   metallo-endopeptidase involved in the extracellular metabolism of
RT   neuropeptides in Aplysia californica.";
RL   J. Neurosci. 19:4280-4292(1999).
DR   EMBL; AF104361; AAD51382.1; -.
DR   HSSP; P08473; 1DMT.
DR   InterPro; IPR000718; Peptidase_M13.
DR   InterPro; IPR000130; Zn_MTpeptdse.
DR   Pfam; PF01431; Peptidase_M13; 1.
DR   PRINTS; PR00786; NEPRILYSIN.
DR   PRINTS; PR01651; SECGEXPORT.
DR   PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
SQ   SEQUENCE   787 AA;  88171 MW;  3D91D1485CECE437 CRC64;

  Query Match             30.9%;  Score 1223;  DB 5;  Length 787;
  Best Local Similarity   35.6%;  Pred. No. 3e-76;
  Matches  271;  Conservative  147;  Mismatches  289;  Indels   54;  Gaps   16;

Qy      2 EAETGSSVETGKKANRGTRIALVVFVGGTLVLGTILFLVSQGLLSLQAKQEYCLKPECIE 61
          |  :||   |   :  |   :     |||                 |  :  :  |:   |:
Db     68 EPSSGSDGTTSAASGSGGTTSAASGSGGT-------------TSADSDGKICVHEGCVT 113

Qy     62 AAAAILSKVNLSVDPCDNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLEK 121
          ||| |:| :: || ||||||: |||  |  :  ||:|  :  |   |   || ::| ::|
Db    114 AAARIMSNLDKSVHPCDNFYNFACANWEYDRDIPKDSAALSVLSELGKKVDRQVKLIIE- 172

Qy    122 SISRRRDTEAIQKAKILYSSCMNEKAIEKADAKPLLHILRHSPFRWPVLESNIGPEGVWS 181
          : |   :   : ||| || ||:: : ::     |   |  :   ||:: |       ::
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Db    173 APSPPDELPVVTKAKNLYKSCLDLETMDARGIDPYKQWLSSTIGEWPLISS------AFN 226

Qy    182 ERKFSLLQTLATFRGQYSNSVFIRLYVSPDDKASNEHILKLDQATLSLAVREDYL--DNS 239
Db    227 ESEFDITDAIRK-ANIYGPGPVVAFYVGTDDKNSSKKILKIDQPAFGLPGQRYYRVPRND 285

Qy    240 TEAKSYRDALYKFMVDTAVLLG-ANSSRAEHDMKSVLRLEIKIAEIMI-PHENRTSEAMY 297
Db    286 TYIKAYETYLYR----VAEALGFADPATAEKDVADVVDFEMQIAQISVRPAIRRNANAVF 341

Qy    298 NKMNISELSA--MIPQFDWLGYIKKVIDTRLYPHLK-DISPSENVVVRVPQYFKDLFRIL 354
Db    342 NPMTLAELDQDFSSPELNFSRLITTVMSA---PEVAVSVGDDEIIMNRSPPYFRNLTDLL 398

Qy    355 GSERKKTIANYLVWRMVYSRIPNLSRRFQYRWLEFSRVIQGTTTLLPQWDKCVNFIESAL 414
Db    399 RNTPKKTIANYIIWRITISYLGTLTQVFKDIRFEFTKAIYGIETVQPRELFCTSFVRRNV 458

Qy    415 PYVVGKMFVDVYFQEDKKEMMEELVEGVRWAFIDMLEKENEWMDAGTKRKAKEKARAVLA 474
Db    459 GFIISKPFVDKFFSPEAKDVALEMISGLQSAFNEIVD-EVEWMDEETKVVAREKNDAIVS 517

Qy    475 KVGYPEFIMNDTHVNEDLKAIKFSEADYFGNVLQTRKYLAQSDFFWLRKAVPKTEWFTNP 534
Db    518 KIGYPEFVINSTRLTELYENYTYGNDTYFENILSKNKVNVDSSFRSLRELVDKEQWFRSP 577

Qy    535 TTVNAFYSASTNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNGRKYD 594
Db    578 PTVNAYYNKAGNEIVFPAGILQSPVF-HVDFPKYLNYGSIGVIIGHEITHGFDDKGRLYD 636

Qy    595 KNGNLDPWWSTESEEKFKEKTKCMINQYSNYYWKKAGLNVKGKRTLGENIADNG------ 648
Db    637 KNGNLNQWWSNSAIEKFNTQKQCIIDQYGAYVMDQVELNLNGIRTQGENIADNGVSKSLS 696

Qy    649 GLREAFRAYRKWINDRRQGLEEPLLPGITFTNNQLFFLSYAHVRCNSYRPEAAREQVQIG 708
Db    697 GRTKLGQSTRK---------EEPTLPGLQYTNDQLFFISFGQTWCNMYRNDALISSIRSG 747

Qy    709 AHSPPQFRVNGAISNSEEFQKAFNCPPNSTMNRGMDSCRLW 749
Db    748 VHSPGQYRVIGSLQNSEDFARVFNCPSTSYMN-AANKCQVW 787


RESULT 13
Q9BLH1
ID   Q9BLH1      PRELIMINARY;      PRT;   772 AA.
AC   Q9BLH1;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Neutral endopeptidase 24.11.
GN   BMNEP-L.
OS   Bombyx mori (Silk moth).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC   Bombycoidea; Bombycidae; Bombyx.
OX   NCBI_TaxID=7091;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Kawasaki H., Zhao X.;
RL   Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Zhao X., Mita K., Shimada T., Okano K., Quan G., Kanke E.;
RT   "Isolation of a 20-hydroxyecdysone inducible neprilysin (neutral
RT   endopeptidase 24.11)-like gene and its expression in wing discs during
RT   metamorphosis of Bombyx mori.";
RL   Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB048208; BAB33300.1; -.
DR   HSSP; P08473; 1DMT.
DR   InterPro; IPR000718; Peptidase_M13.
DR   InterPro; IPR001230; Prenyl_site.
DR   InterPro; IPR000130; Zn_MTpeptdse.
DR   Pfam; PF01431; Peptidase_M13; 1.
DR   PRINTS; PR00786; NEPRILYSIN.
DR   PROSITE; PS00294; PRENYLATION; UNKNOWN_1.
DR   PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
SQ   SEQUENCE   772 AA;  87763 MW;  B0D5338EAF4F0D56 CRC64;

  Query Match           30.8%;  Score 1219;  DB 5;  Length 772;
  Best Local Similarity   37.6%;  Pred. No. 5.5e-76;
  Matches  264;  Conservative  137;  Mismatches  276;  Indels   26;  Gaps   16;

Qy     52 EYCLKPECIEAAAAILSKVNLSVDPCDNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNV 111
Db     91 ETCSAPGCIHTASRLLLNMDEKVDPCDNFYDFACGSFLKNTRIPGDKTSVNTFSIITDQL 150

Qy    112 DLKLKELLEKSISRRRDTEAIQKAKILYSSCMNEKAIEKADAKPLLHILRHSPFRWPVLE 171
Db    151 QEQIRSLLDEPVT-PEEPRPFVLAKTLYQACMNRTAIEARGVQPLLDMLKRLG-GWPVLD 208

Qy    172 SNIGPEGVWSERKFSLLQTLATFR-GQYSNSVFIRLYVSPDDKASNEHILKLDQATLSLA 230
Db    209 GQ-----SWDENSFSWEQSVYKFRDAGYSVDYFLDFSISVDVKNSTRRVIDLDQASLGLS 263

Qy    231 VREDYLDNSTEAKSYRDALYKFMVDTAVLLGANSSRAEHDMKSVLRLEIKIAEIMIPHE- 289
Db    264 --REYLNRGFSDKLVQ-AYYEYMVDIAILLGADKTKATEELKESLQFEMKLANISLPLEK 320

Qy    290 NRTSEAMYNKMNISELSAMIPQFDWLGYIKKVIDTRLYPHLKDISPSENVVVRVPQYFKD 349
Db    321 RRNATSLYNPMTIAELQQKFPKVPWLEYINRL----LAPHI-TVDVNELTIVSVPKYITD 375

Qy    350 LFRILGSERKKTIANYLVWRMVYSRIPNLSRRFQYRWLEFSRVIQGTTTLLPQWDKCVNF 409
Db    376 LEALLEKTPKRVQANYVMWRVAGASVSYLTDDLRRRQLAYITALSGKTERESRWKECADT 435

Qy    410 IESALPYVVGKMFVDVYFQEDKKEMMEELVEGVRWAFIDMLEKENEWMDAGTKRKAKEKA 469
Db    436 TSASMSIAVGALYIRKYFNENSKANALEMVNDIRQQFRKTLTKV-DWMDDMTRQEALEKA 494

Qy    470 RAVLAKVGYPEFIMNDTHVNEDLKAIKFSEADYFGNVLQTRKYLAQSDFFWLRKAVPKTE 529
Db    495 DAMASHIAYPSEMLDNNRLTEFYSGLEMSSEHLMESVLNLTLFTTEYLFGKLREPVNKTD 554

Qy    530 WFTN--PTTVNAFYSASTNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFD 587
Db    555 WVTHGRPAIVNAFYSSIENSIQFPAGILQGAFF-SAKRPAYMNYGAIGFVIGHEITHGFD 613

Qy    588 NNGRKYDKNGNLDPWWSTESEEKFKEKTKCMINQYSNYYWKKAGLNVKGKRTLGENIADN 647
Db    614 DQGRQFDKNGNLVDWWQEMTKEKYLDKAKCIIDQYSNYTVKEVGLKLNGVNTQGENIADN 673

Qy    648 GGLREAFRAYRKWINDRRQGLEEPLLPGI-TFTNNQLFFLSYAHVRCNSYRPEAAREQVQ 706
Db    674 GGIKEAYYAYQAWTH--RHG-EEARLPGLEKYSPRQLFWLSAANTWCAVYRNEAIKLRIT 730

Qy    707 IGAHSPPQFRVNGAISNSEEFQKAFNCPPNSTMNRGMDSCRLW 749
Db    731 TGFHAPGRFRVIGPMSNMEEFASDFKCPMGSPMNPD-KKCKVW 772


RESULT 14
O16796
ID   O16796      PRELIMINARY;      PRT;   848 AA.
AC   O16796;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Hypothetical 97.1 kDa protein.
GN   F18A12.8.
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
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RP   SEQUENCE FROM N.A.
RC   STRAIN=BRISTOL N2;
RX   MEDLINE=99069613; PubMed=9851916;
RA   None;
RT   "Genome sequence of the nematode C. elegans: a platform for
RT   investigating biology. The C. elegans Sequencing Consortium.";
RL   Science 282:2012-2018(1998).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BRISTOL N2;
RA   Waterston R., Ozersky P., Le T.T.;
RT   "The sequence of C. elegans cosmid F18A12.";
RL   Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BRISTOL N2;
RA   Waterston R.;
RT   "Direct Submission.";
RL   Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF016688; AAB66079.2; -.
DR   HSSP; P08473; 1DMT.
DR   InterPro; IPR000718; Peptidase_M13.
DR   InterPro; IPR001230; Prenyl_site.
DR   InterPro; IPR000130; Zn_MTpeptdse.
DR   Pfam; PF01431; Peptidase_M13; 1.
DR   PRINTS; PR00786; NEPRILYSIN.
DR   PROSITE; PS00294; PRENYLATION; UNKNOWN_1.
DR   PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   848 AA;  97061 MW;  4548FFEE5A915DA4 CRC64;

  Query Match             30.5%;  Score 1209;  DB 5;  Length 848;
  Best Local Similarity   35.4%;  Pred. No. 3.1e-75;
  Matches  254;  Conservative  140;  Mismatches  277;  Indels   46;  Gaps   15;

Qy      52 EYCLKPECIEAAAAILSKVNLSVDPCDNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNV 111
Db     159 EVCSTPGCVRAATHFLNAMNTSVDPCDDFFEFACGQWNDQHPIPDDMYGFGTFAYAREQV 218

Qy     112 DLKLKELLEKSISRRRDTEAIQKAKILYSSCMNEKAIEKADAKPLLHILRHSPFRWPVLE 171
Db     219 RQQLRVLLEQEVV--TESESINMARATYRSCMNKTQLDELMTGPLFETLTELG-EWPLLQ 275

Qy     172 SNIGPEGVWSERKFSLLQTLATFRGQYSNSVFIRLYVSPDDKASNEHILKLDQATLSLA- 230
Db     276 EN------WDKTKFNFTSLLVNSRRDYGVDVFFQLYIYADSKNTSRNTLFIDQSTLALGR 329

Qy     231 VREDYLDNSTEAKSYRDALYKFMVDTAVLL--GANSSRAEH----DMKSVLRLEIKIAEI 284
Db     330 GTRDYYLNTTLFSSHMTAYRKYLRQIAHLLKTDGNLTRSESEMNADIEKIIDFEIELAKI 389

Qy     285 MIPH-ENRTSEAMYNKMNISELSAMIPQFDWLGYIKKVIDTRLYPHLKDISPSE------ 337
Db     390 IVAEDERRNNTRLYNKRQIQDLYNLLPQVDWV-----------PFFQSIAPSDLTHLFH 437

Qy     338 ---NVVVRVPQYFKDLFRILGSERKKTIANYLVWRMVYSRIPNLSRRFQYRWLEFSRVIQ 394
Db     438 NETEIIICEIEYLQHVSELIEKTDVGLLTNYVLWRVVQSNVRYLDERFEDIKQDFLKVMT 497

Qy     395 GTTTLLPQWDKCVNFIESALPYVVGKMFVDVYFQEDKKEMMEELVEGVRWAFIDMLEKEN 454
Db     498 GQQQSPPRWKDCAQVPSTVLPLAAGAIYVQAHFQESDKHEALRMIMHLRNSFADLV-RQN 556

Qy     455 EWMDAGTKRKAKEKARAVLAKVGYPEFIMNDTHVNEDLKAIKFSEADYFGNVLQTRKYLA 514
Db     557 DWMDEETKAVAIEKANSMINNIGYPDVTNDLPKLDKQYLGLSISDSDTYYYIMKKSVVWM 616

Qy     515 QS-DFFWLRKAVPKTEWFTNPTTVNAFYSASTNQIRFPAGELQKPFFWGTEYPRSLSYGA 573
Db     617 QSREFQKLTKPFDKHEFDISPAVVNAFYSPEKNAITFPAGILQPPFFSGT-FPKAVNYGA 675

Qy     574 IGVIVGHEFTHGFDNNGRKYDKNGNLDPWWSTESEEKFKEKTKCMINQYSNYYWKKAGLN 633
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Db     676 IGAVIGHEITHGFDDQGSQYDKDGNLHNWWSESSLNSFDTRRRCIVEQYGNYTVPKTNFR 735

Qy     634 VKGKRTLGENIADNGGLREAFRAYRKWINDRRQGLEEPLLPGI-TFTNNQLFFLSYAHVR 692
Db     736 VNGKLTQGENIADNGGVKEAFQAYQKYVTENG---EEPRLPGLQQYTNEQIFFVSYAHFW 792

Qy     693 CNSYRPEAAREQVQIGAHSPPQFRVNGAISNSEEFQKAFNCPPNSTMNRGMDSCRLW 749
Db     793 CGKKKEAAAMQQVLTDEHSPEVFRVIGVLSNMQAFADVYKCPRNAPVNPD-HKCIVW 848


RESULT 15
Q923T6
ID   Q923T6      PRELIMINARY;      PRT;   763 AA.
AC   Q923T6;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Endothelin converting enzyme-2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL;
RA   Pan H., Mzhavia N., Devi L.A.;
RT   "Mouse Endothelin Converting Enzyme-2 cDNA.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF396699; AAK83919.1; -.
DR   MEROPS; M13.003; -.
DR   InterPro; IPR000718; Peptidase_M13.
DR   InterPro; IPR000221; Protamine_P1.
DR   InterPro; IPR000130; Zn_MTpeptdse.
DR   Pfam; PF01431; Peptidase_M13; 1.
DR   PROSITE; PS00048; PROTAMINE_P1; UNKNOWN_1.
DR   PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
SQ   SEQUENCE   763 AA;  86205 MW;  4B518B0EEF9BE549 CRC64;

  Query Match             30.5%;  Score 1208;  DB 11;  Length 763;
  Best Local Similarity   35.4%;  Pred. No. 3.1e-75;
  Matches  267;  Conservative  134;  Mismatches  312;  Indels   42;  Gaps   16;

Qy       4 ETGSSVETGKKANRGTRIALV----VFVGGTLVLGTILFLVSQGLLSLQAKQEYCLKPEC 59
Db      42 EVGFQKRTRQLFGSHTQLELVLAGLILVLAALLLGCLVAL----WVHRDPAHSTCVTEAC 97

Qy      60 IEAAAAILSKVNLSVDPCDNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELL 119
Db      98 IRVAGKILESLDRGVSPCQDFYQFSCGGWIRRNPLPNGRSRWNTFNSLWDQNQAILKHLL 157

Qy     120 EKSISRRRDTEAIQKAKILYSSCMNEKAIEKADAKPLLHILRHSPFRWPVLESNIGP--- 176
Db     158 ENT-TFNSSSEAERKTRSFYLSCLQSERIEKLGAKPLRDLI-----------DKIGGWNI 205

Qy     177 EGVWSERKFSLLQTLATFRGQYSNSVFIRLYVSPDDKASNEHILKLDQATLSLAVREDYL 236
Db     206 TGPWDEDSF--MDVLKAVAGTYRATPFFTVYVSADSKSSNSNIIQVDQSGLFLPSRDYYL 263

Qy     237 DNSTEAKSYRDALYKFMVDTAVLLGANSSRAEHDMKSVLRLEIKIAEIMIPH-ENRTSEA 295
Db     264 -NRTANEKVLTAYLDYMVELGVLLGGQPTSTREQMQQVLELEIQLANITVPQDQRRDEEK 322

Qy     296 MYNKMNISELSAMIPQFDWLGYIKKVIDTRLYPHLKDISPSENVVVRVPQYFKDLFRILG 355
Db     323 IYHKMSISELQALAPAVDWLEFLSFLLSP-----LELGDSEPVVVYGTEYLQQVSELIN 376

Qy     356 SERKKTIANYLVWRMVYSRIPNLSRRFQYRWLEFSRVIQGT-TTLLPQWDKCVNFIESAL 414
Db     377 RTEPSILNNYLIWNLVQKTTSSLDQRFETAQEKLLETLYGTKKSCTPRWQTCISNTDDAL 436

Qy     415 PYVVGKMFVDVYFQEDKKEMMEELVEGVRWAFIDMLEKENEWMDAGTKRKAKEKARAVLA 474
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Db    437 GFALGSLFVKATFDRQSKEIAEGMINEIRSAFEETL-GDLVWMDEKTRLAAKEKADAIYD 495

Qy    475 KVGYPEFIMNDTHVNEDLKAIKFSEADYFGNVLQTRKYLAQSDFFWLRKAVPKTEWFTNP 534
          :|:|:||:    :::     : ||  :| |:|    : |:     |||   : :|   |
Db    496 MIGFPDFILEPKELDDVYDGYEVSEDSFFQNMLNLYNFSAKVMADQLRKPPSRDQWSMTP 555

Qy    535 TTVNAFYSASTNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNGRKYD 594
          ||||:|  : |:| |||| || ||     :|::|::| |||::||| || ||: ||:||
Db    556 QTVNAYYLPTKNEIVFPAGILQAPFH-AHNHPKALNFGGIGVVMGHELTHAFDDQGREYD 614

Qy    595 KNGNLDPWWSTESEEKFKEKTKCMINQYSNYYWKKAGLNVKGKRTLGENIADNGGLREAF 654
          | ||| ||| || |: | || ||| |  :  |  : | :||||||||||||: |:
Db    615 KEGNLRPWWQNESLTAFQNHTACMEEQYSQY--QVNGERLNGLQTLGENIADNGGLKAAY 672

Qy    655 RAYRKWINDRRQGLEEPLLPGITFTNNQLFFLSYAHVRCNSYRPEAAREQVQIGAHSPPQ 714
          ||: |:  |: | |:| || :  ||:|||| : | |:   ||:: | :    ||| :
Db    673 NAYKAWL--RKHGEEQP-LPAVGLTNHQLFFVGFAQVWCSVRTPESSHEGLVTDPHSPAR 729

Qy    715 FRVNGAISNSEEFQKAFNCPPNSTMNRGMDSCRLW 749
          ||| | :||| :| : | ||  | || |   | :|
Db    730 FRVLGTLSNSRDFLRHFGCPVGSPMNPG-QLCEVW 763

Search completed: May 21, 2003, 18:49:07
Job time : 46 secs
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GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

Run on: May 21, 2003, 18:39:14 ; Search time 79 Seconds
(without alignments)
1263.351 Million cell updates/sec

Title: US-09-913-955A-1
Perfect score: 3958
Sequence: 1 MEAETGSSVETGKKANRGTR.....AFNCPPNSTMNRGMDSCRLW 749

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_101002:*
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2: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
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22: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3958	100.0	749	21	AAY96190	Human PHEX. Homo
2	3952	99.8	749	21	AAY84627	Amino acid sequenc
3	3928	99.2	749	19	AAW53457	Amino acid sequenc
4	1375.5	34.8	765	21	AAB08130	A murine neutral e
5	1362	34.4	753	22	AAB60562	Human neprilysin-l
6	1352	34.2	753	22	AAB83842	Amino acid sequenc
7	1351	34.1	774	20	AAY44177	Rat membrane metal
8	1343.5	33.9	779	22	AAB60561	Human neprilysin-l
9	1333.5	33.7	779	22	AAB83841	Amino acid sequenc
10	1332.5	33.7	770	21	AAB08131	A human neutral en
11	1332.5	33.7	779	23	ABB79521	Human SEP endopept
12	1332.5	33.7	779	23	AAU78850	Novel neprilysin f
13	1332.5	33.7	779	23	AAE17779	Human soluble secr
14	1326.5	33.5	702	22	AAB83844	Amino acid sequenc
15	1322.5	33.4	691	22	AAB83840	Amino acid sequenc
16	1321	33.4	742	23	AAE19176	Human protease, PR
17	1317	33.3	746	23	AAE17781	Soluble secreted e
18	1310.5	33.1	743	23	AAU72903	Human metalloprote
19	1283.5	32.4	743	22	AAE07916	Human neutral endo
20	1283.5	32.4	743	22	AAE07952	Human neutral endo
21	1283.5	32.4	743	22	AAB85104	Human enkephalinas
22	1283.5	32.4	743	22	AAB85115	Human enkephalinas
23	1283.5	32.4	748	15	AAR52706	Human enkephalinas
24	1275.5	32.2	750	10	AAP90393	Human common acute
25	1270.5	32.1	748	9	AAP80969	Enkephalinase (hum
26	1270	32.1	762	22	AAB60563	Human neprilysin-l
27	1265.5	32.0	750	9	AAP82940	Atrial natriuretic
28	1263.5	31.9	750	9	AAP82867	Enkephalinase (rat
29	1263.5	31.9	750	15	AAR52707	Rat enkephalinase.
30	1257	31.8	703	16	AAR76237	Human placental en
31	1257	31.8	753	16	AAR75691	Endothelin convert
32	1257	31.8	753	16	AAR76227	Human endothelin c
33	1257	31.8	753	23	ABG65798	Human Endothelin c
34	1257	31.8	758	17	AAW03682	Human endothelin c
35	1257	31.8	758	17	AAW03736	Human endothelin c
36	1256	31.7	753	23	ABG65799	Human Endothelin c
37	1248.5	31.5	758	19	AAW38369	Bovine endothelin
38	1241.5	31.4	708	16	AAR76236	Bovine foetal hear
39	1241.5	31.4	754	16	AAR76226	Bovine endothelin
40	1223	30.9	736	20	AAY41774	Human PRO403 prote
41	1223	30.9	736	21	AAB44330	Human PRO403 prote
42	1223	30.9	736	22	AAU29233	Human PRO polypept
43	1221	30.8	883	22	AAB67845	Polypeptide homolo
44	1212	30.6	766	23	AAU82722	Amino acid sequenc
45	1205.5	30.5	661	22	ABB61898	Drosophila melanog

ALIGNMENTS

RESULT 1
AAY96190
ID AAY96190 standard; protein; 749 AA.
XX
AC AAY96190;
XX
DT 19-DEC-2000 (first entry)
XX
DE Human PHEX.
XX
KW PHEX; human; metalloprotease; endopeptidase; X chromosome;
KW X-linked hypophosphatemia; hyperphosphatemia; hyperparathyroidism;
KW renal osteodystrophy; phosphaturia; therapy; diagnosis.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 21..40
FT /label= Transmembrane_domain
XX
PN WO200050580-A2.
XX
PD 31-AUG-2000.
XX
PF 24-FEB-2000; 2000WO-CA00201.
XX
PR 24-FEB-1999; 99CA-2262056.
XX
PA (UYMO-) UNIV MONTREAL.
XX
PI Crine P, Boileau G;
XX
DR WPI; 2000-565455/52.

```
XX
PT   Novel soluble human PHEX enzyme useful for treating phosphaturia and/or
PT   hypophosphatemia, is a gene product of phosphate-regulating gene having
PT   homology to endopeptidase on X chromosome -
XX
PS   Disclosure; Fig 2; 64pp; English.
XX
CC   The present sequence is that of human PHEX (a gene product of
CC   phosphate-regulating gene with homology to endopeptidase on X
CC   chromosome). Absence of a functioning PHEX gene is associated with
CC   hypophosphatemia. PHEX is a type II integral membrane glycoprotein.
CC   To produce a soluble form of PHEX, the transmembrane anchor domain
CC   was modified with a signal peptidase coding sequence (see AAY96188
CC   and AAY96189). The soluble PHEX thus comprised the active ectodomain.
CC   An inactive PHEX can also constructed by replacement of the
CC   Glu-582 residue by a hydrophobic amino acid residue, especially
CC   valine. Soluble and inactive mutant forms of PHEX can be used to
CC   screen ligands to PHEX. These ligands are used as substrates
CC   or inhibitors of PHEX. Since PHEX is phosphaturic, an inhibitor
CC   can be used to treat phosphaturia and/or hypophosphatemia. A
CC   substrate for PHEX, or PHEX itself, can be used to treat
CC   hyperphosphatemia, including its most frequent manifestations,
CC   secondary hyperparathyroidism and renal osteodystrophy.
XX
SQ   Sequence   749 AA;

  Query Match           100.0%;  Score 3958;  DB 21;  Length 749;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  749;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MEAETGSSVETGKKANRGTRIALVVFVGGTLVLGTILFLVSQGLLSLQAKQEYCLKPECI 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MEAETGSSVETGKKANRGTRIALVVFVGGTLVLGTILFLVSQGLLSLQAKQEYCLKPECI 60

Qy      61 EAAAAILSKVNLSVDPCDNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLE 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 EAAAAILSKVNLSVDPCDNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLE 120

Qy     121 KSISRRRDTEAIQKAKILYSSCMNEKAIEKADAKPLLHILRHSPFRWPVLESNIGPEGVW 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 KSISRRRDTEAIQKAKILYSSCMNEKAIEKADAKPLLHILRHSPFRWPVLESNIGPEGVW 180

Qy     181 SERKFSLLQTLATFRGQYSNSVFIRLYVSPDDKASNEHILKLDQATLSLAVREDYLDNST 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 SERKFSLLQTLATFRGQYSNSVFIRLYVSPDDKASNEHILKLDQATLSLAVREDYLDNST 240

Qy     241 EAKSYRDALYKFMVDTAVLLGANSSRAEHDMKSVLRLEIKIAEIMIPHENRTSEAMYNKM 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 EAKSYRDALYKFMVDTAVLLGANSSRAEHDMKSVLRLEIKIAEIMIPHENRTSEAMYNKM 300

Qy     301 NISELSAMIPQFDWLGYIKKVIDTRLYPHLKDISPSENVVVRVPQYFKDLFRILGSERKK 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 NISELSAMIPQFDWLGYIKKVIDTRLYPHLKDISPSENVVVRVPQYFKDLFRILGSERKK 360

Qy     361 TIANYLVWRMVYSRIPNLSRRFQYRWLEFSRVIQGTTTLLPQWDKCVNFIESALPYVVGK 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 TIANYLVWRMVYSRIPNLSRRFQYRWLEFSRVIQGTTTLLPQWDKCVNFIESALPYVVGK 420

Qy     421 MFVDVYFQEDKKEMMEELVEGVRWAFIDMLEKENEWMDAGTKRKAKEKARAVLAKVGYPE 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 MFVDVYFQEDKKEMMEELVEGVRWAFIDMLEKENEWMDAGTKRKAKEKARAVLAKVGYPE 480

Qy     481 FIMNDTHVNEDLKAIKFSEADYFGNVLQTRKYLAQSDFFWLRKAVPKTEWFTNPTTVNAF 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 FIMNDTHVNEDLKAIKFSEADYFGNVLQTRKYLAQSDFFWLRKAVPKTEWFTNPTTVNAF 540

Qy     541 YSASTNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNGRKYDKNGNLD 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 YSASTNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNGRKYDKNGNLD 600

Qy     601 PWWSTESEEKFKEKTKCMINQYSNYYWKKAGLNVKGKRTLGENIADNGGLREAFRAYRKW 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 PWWSTESEEKFKEKTKCMINQYSNYYWKKAGLNVKGKRTLGENIADNGGLREAFRAYRKW 660

Qy     661 INDRRQGLEEPLLPGITFTNNQLFFLSYAHVRCNSYRPEAAREQVQIGAHSPPQFRVNGA 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 INDRRQGLEEPLLPGITFTNNQLFFLSYAHVRCNSYRPEAAREQVQIGAHSPPQFRVNGA 720

Qy     721 ISNSEEFQKAFNCPPNSTMNRGMDSCRLW 749
           |||||||||||||||||||||||||||||
Db     721 ISNSEEFQKAFNCPPNSTMNRGMDSCRLW 749


RESULT 2
AAY84627
ID   AAY84627 standard; Protein; 749 AA.
XX
AC   AAY84627;
XX
DT   25-JUL-2000  (first entry)
XX
DE   Amino acid sequence of a human PEX protein.
XX
KW   Human; PEX gene; Xp22.1; X-linked hypophosphatemic rickets; osteoblast;
KW   parathyroid hormone; PTH; osteoclast; bone; bone breakdown;
KW   parathyroid hormone related peptide; PTHrP; metabolic bone disease;
KW   osteomalacia; osteoporosis; osteopetrosis; Paget's disease.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   71
FT                   /note= "potential N-glycosylation site"
FT   Modified-site   238
FT                   /note= "potential N-glycosylation site"
FT   Modified-site   263
FT                   /note= "potential N-glycosylation site"
FT   Modified-site   290
FT                   /note= "potential N-glycosylation site"
FT   Modified-site   301
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FT   Modified-site   484
FT                   /note= "potential N-glycosylation site"
FT   Modified-site   726
FT                   /note= "putative prenylation site"
FT   Modified-site   736
FT                   /note= "potential N-glycosylation site"
XX
PN   WO200018954-A2.
XX
PD   06-APR-2000.
XX
PF   27-SEP-1999;   99WO-CA00895.
XX
PR   28-SEP-1998;   98CA-2245903.
XX
PA   (UYMC-) UNIV MCGILL.
XX
PI   Karaplis AC,  Goltzman D,  Lipman ML,  Henderson JE;
XX
DR   WPI; 2000-293177/25.
DR   N-PSDB; AAA12670.
XX
PT   Diagnosis and treatment of metabolic bone diseases e.g. osteomalacia
PT   and osteoporosis comprises determining the level of parathyroid hormone
PT   related peptide in a patient -
XX
PS   Disclosure; Fig 2A; 52pp; English.
XX
CC   The present sequence is encoded by the human PEX gene. The PEX gene spans
CC   the deleted region Xp22.1 in X-linked hypophosphatemic rickets. The gene
CC   is mutated in non-deletion patients with the disorder. PEX is a cell
CC   membrane-associated protein with its active site in the extracellular
CC   compartment. The cells with the highest level of PEX expression are the
```

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CC   osteoblasts. These cells are also the site of action of circulating
CC   parathyroid hormone (PTH). PTH stimulates these cells to produce factors
CC   which in turn stimulate other bone cells, specifically osteoclasts, to
CC   break down bone. Since PEX likely inactivates PTH in contact with
CC   osteoblasts, it results in decreased stimulation of osteoclasts and
CC   therefore bone breakdown. Parathyroid hormone related peptide (PTHrP)
CC   may also serve as a substrate for PEX. PTH and PTHrP levels can be
CC   modulated using PEX. This regulates osteoblast activity, and can be
CC   used for the treatment and diagnosis of metabolic bone diseases which
CC   include osteomalacia, osteoporosis, osteopetrosis or Paget's disease.
XX
SQ   Sequence   749 AA;

  Query Match           99.8%;  Score 3952;  DB 21;  Length 749;
  Best Local Similarity 99.9%;  Pred. No. 0;
  Matches  748;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 MEAETGSSVETGKKANRGTRIALVVFVGGTLVLGTILFLVSQGLLSLQAKQEYCLKPECI 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MEAETGSSVETGKKANRGTRIALVVFVGGTLVLGTILFLVSQGLLSLQAKQEYCLKPECI 60

Qy      61 EAAAAILSKVNLSVDPCDNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLE 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 EAAAAILSKVNLSVDPCDNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLE 120

Qy     121 KSISRRRDTEAIQKAKILYSSCMNEKAIEKADAKPLLHILRHSPFRWPVLESNIGPEGVW 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 KSISRRRDTEAIQKAKILYSSCMNEKAIEKADAKPLLHILRHSPFRWPVLESNIGPEGVW 180

Qy     181 SERKFSLLQTLATFRGQYSNSVFIRLYVSPDDKASNEHILKLDQATLSLAVREDYLDNST 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 SERKFSLLQTLATFRGQYSNSVFIRLYVSPDDKASNEHILKLDQATLSLAVREDYLDNST 240

Qy     241 EAKSYRDALYKFMVDTAVLLGANSSRAEHDMKSVLRLEIKIAEIMIPHENRTSEAMYNKM 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 EAKSYRDALYKFMVDTAVLLGANSSRAEHDMKSVLRLEIKIAEIMIPHENRTSEAMYNKM 300

Qy     301 NISELSAMIPQFDWLGYIKKVIDTRLYPHLKDISPSENVVVRVPQYFKDLFRILGSERKK 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 NISELSAMIPQFDWLGYIKKVIDTRLYPHLKDISPSENVVVRVPQYFKDLFRILGSERKK 360

Qy     361 TIANYLVWRMVYSRIPNLSRRFQYRWLEFSRVIQGTTTLLPQWDKCVNFIESALPYVVGK 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 TIANYLVWRMVYSRIPNLSRRFQYRWLEFSRVIQGTTTLLPQWDKCVNFIESALPYVVGK 420

Qy     421 MFVDVYFQEDKKEMMEELVEGVRWAFIDMLEKENEWMDAGTKRKAKEKARAVLAKVGYPE 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 MFVDVYFQEDKKEMMEELVEGVRWAFIDMLEKENEWMDAGTKRKAKEKARAVLAKVGYPE 480

Qy     481 FIMNDTHVNEDLKAIKFSEADYFGNVLQTRKYLAQSDFFWLRKAVPKTEWFTNPTTVNAF 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 FIMNDTHVNEDLKAIKFSEADYFGNVLQTRKYLAQSDFFWLRKAVPKTEWFTNPTTVNAF 540

Qy     541 YSASTNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNGRKYDKNGNLD 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 YSASTNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNGRKYDKNGNLD 600

Qy     601 PWWSTESEEKFKEKTKCMINQYSNYYWKKAGLNVKGKRTLGENIADNGGLREAFRAYRKW 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 PWWSTESEEKFKEKTKCMINQYSNYYWKKAGLNVKGKRTLGENIADNGGLREAFRAYRKW 660

Qy     661 INDRRQGLEEPLLPGITFTNNQLFFLSYAHVRCNSYRPEAAREQVQIGAHSPPQFRVNGA 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 INDRRQGLEEPLLPGITFTNNQLFFLSYAHVRCNSYRPEAAREQVQIGAHSPPQFRVNGA 720

Qy     721 ISNSEEFQKAFNCPPNSTMNRGMDSCRLW 749
           ||| ||||||||||||||||||||||||||
Db     721 ISNFEEFQKAFNCPPNSTMNRGMDSCRLW 749


RESULT 3
AAW53457
ID   AAW53457 standard; Protein; 749 AA.
XX
AC   AAW53457;
XX
DT   28-JUL-1998  (first entry)
XX
DE   Amino acid sequence of human tumour PEX protein.
XX
KW   Recombinant tumour PEX protein; phosphate regulating gene; inhibition;
KW   endopeptidases; metalloendopeptidase; tumour; OHO; PEX active site;
KW   oncogenous hypophosphataemia osteomalacia; chronic renal failure;
KW   idiopathic hypercalcuria.
XX
OS   Homo sapiens.
XX
PN   WO9810078-A2.
XX
PD   12-MAR-1998.
XX
PF   04-SEP-1997;   97WO-CA00617.
XX
PR   05-SEP-1996;   96US-0025454.
XX
PA   (GOLT/) GOLTZMAN D.
PA   (HEND/) HENDERSON J E.
PA   (KARA/) KARAPLIS A C.
PA   (LIPM/) LIPMAN M L.
PA   (PAND/) PANDA D.
PA   (SHEN/) SHEN Y.
XX
PI   Goltzman D,  Henderson JE,  Karaplis AC,  Lipman ML;
PI   Panda D,  Shen Y;
XX
DR   WPI; 1998-193628/17.
DR   N-PSDB; AAV23264.
XX
PT   DNA encoding human PEX - useful for the treatment of
PT   hyper:phosphataemia or chronic renal failure
XX
PS   Disclosure; Fig 1A-1G; 27pp; English.
XX
CC   This is the amino acid sequence of the recombinant human tumour PEX
CC   protein a product of a phosphate regulating gene with homology to
CC   endopeptidases, suggesting that PEX might be a metalloendopeptidase.
CC   It was isolated from tumours causing oncogenous hypophosphataemia
CC   osteomalacia (OHO).  Compounds which are targeted to inhibit PEX
CC   active site, identified in the method of the invention, are useful
CC   for the treatment of hyperphosphataemia or chronic renal failure.
CC   PEX can also be used as a target for the treatment of idiopathic
CC   hypercalcuria.
XX
SQ   Sequence   749 AA;

  Query Match           99.2%;  Score 3928;  DB 19;  Length 749;
  Best Local Similarity 99.5%;  Pred. No. 0;
  Matches  745;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 MEAETGSSVETGKKANRGTRIALVVFVGGTLVLGTILFLVSQGLLSLQAKQEYCLKPECI 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MEAETGSSVETGKKANRGTRIALVVFVGGTLVLGTILFLVSQGLLSLQAKQEYCLKPECI 60

Qy      61 EAAAAILSKVNLSVDPCDNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLE 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 EAAAAILSKVNLSVDPCDNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLE 120

Qy     121 KSISRRRDTEAIQKAKILYSSCMNEKAIEKADAKPLLHILRHSPFRWPVLESNIGPEGVW 180
           |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db     121 KSISRRRDTEAIQKAKILYSSCMNEKAIEKADGKPLLHILRHSPFRWPVLESNIGPEGVW 180

Qy     181 SERKFSLLQTLATFRGQYSNSVFIRLYVSPDDKASNEHILKLDQATLSLAVREDYLDNST 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 SERKFSLLQTLATFRGQYSNSVFIRLYVSPDDKASNEHILKLDQATLSLAVREDYLDNST 240

Qy     241 EAKSYRDALYKFMVDTAVLLGANSSRAEHDMKSVLRLEIKIAEIMIPHENRTSEAMYNKM 300
```

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Db    241 EAKSYRDALYKFMVDTAVLLGANSSRAEHDMKSVLRLEIKIAEIMIPHENRTSEAMYNKM 300

Qy    301 NISELSAMIPQFDWLGYIKKVIDTRLYPHLKDISPSENVVVRVPQYFKDLFRILGSERKK 360
Db    301 NISELSAMIPQFDWLGYIKKVIDTRLYPHLKDISPSENVVVRVPQYFKDLFRILGSERKK 360

Qy    361 TIANYLVWRMVYSRIPNLSRRFQYRWLEFSRVIQGTTTLLPQWDKCVNFIESALPYVVGK 420
Db    361 TIDNYLVWRMVYSRIPNLSRRFQYRWLEFSRVIQGTTTLLPQRDKCVNFIESALPYVVGK 420

Qy    421 MFVDVYFQEDKKEMMEELVEGVRWAFIDMLEKENEWMDAGTKRKAKEKARAVLAKVGYPE 480
Db    421 MFVDVYFQEDKKEMMEELVEGVRWAFIDMLEKENEWMDAGTKRKAKEKARAVLAKVGYPE 480

Qy    481 FIMNDTHVNEDLKAIKFSEADYFGNVLQTRKYLAQSDFFWLRKAVPKTEWFTNPTTVNAF 540
Db    481 FIMNDTHVNEDLKAIKFSEADYFGNVLQTRKYLAQSDFFWLRKAVPKTEWFTNPTTVNAF 540

Qy    541 YSASTNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNGRKYDKNGNLD 600
Db    541 YSASTNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNGRKYDKNGNLD 600

Qy    601 PWWSTESEEKFKEKTKCMINQYSNYYWKKAGLNVKGKRTLGENIADNGGLREAFRAYRKW 660
Db    601 PWWSTESEEKFKEKTKCMINQYSNYYWKKAGLNVKGKRTLGENIADNGGLREAFRAYRKW 660

Qy    661 INDRRQGLEEPLLPGITFTNNQLFFLSYAHVRCNSYRPEAAREQVQIGAHSPPQFRVNGA 720
Db    661 INDRRQGLEEPLLPGITFTNNQLFFLSYAHVRCNSYRPEAAREQVQIGAHSPPQFRVNGA 720

Qy    721 ISNSEEFQKAFNCPPNSTMNRGMDSCRLW 749
Db    721 ISNFEEFQKAFNCPPNSTMNRGMDSCRLW 749
```

RESULT 4
AAB08130
ID AAB08130 standard; Protein; 765 AA.
XX
AC AAB08130;
XX
DT 04-DEC-2000 (first entry)
XX
DE A murine neutral endopeptidase metallopeptidase-like enzyme NL-1.
XX
KW Neprilysin; neutral endopeptidase metallopeptidase-like enzyme;
KW NEP-like enzyme; protein production; protein secretion;
KW neurological disease; Alzheimer's disease; pain; psychiatric disorder;
KW fertility; bone disease; abnormal phosphate metabolism.
XX
OS Mus sp.
XX
PN WO200047750-A2.
XX
PD 17-AUG-2000.
XX
PF 11-FEB-2000; 2000WO-CA00147.
XX
PR 11-FEB-1999; 99CA-2260376.
XX
PA (UYMO-) UNIV MONTREAL.
XX
PI Desgroseillers L, Boileau G;
XX
DR WPI; 2000-549148/50.
DR N-PSDB; AAA63763.
XX
PT Novel neutral endopeptidase-like metallopeptidase polypeptides and
PT polynucleotides, used to screen for related sequences and enzyme
PT inhibitors, used for the treatment of NL-3 related bone disorders -
XX
PS Claim 2; Fig 3; 59pp; English.

XX
CC The present sequence represents a murine neutral endopeptidase
CC metallopeptidase-like enzyme, designated NL-1. The specification
CC also describes NL-2 and NL-3. The NL enzymes are used to test for
CC specific inhibitors. The N-terminal region of the enzymes can be used
CC to promote production and secretion of foreign proteins and active
CC biopeptides, using chimeric constructs containing the foreign protein
CC downstream from and in phase with the N-terminal region. The NL enzymes
CC are have been localised to the brain, and may be useful in the
CC treatment of neurological diseases such as Alzheimer's disease, pain,
CC and psychiatric disorders. NL enzymes have also been localised to the
CC testis and ovaries, and may be used to control fertility. They have
CC also been localised to bones, and may be used to treat bone diseases,
CC and abnormal phosphate metabolisms related to improper peptide
CC processing by the NL-3 enzyme.
XX
SQ Sequence 765 AA;

Query Match 34.8%; Score 1375.5; DB 21; Length 765;
Best Local Similarity 38.8%; Pred. No. 4.7e-109;
Matches 295; Conservative 147; Mismatches 267; Indels 51; Gaps 18;

```
Qy     18 GTRIALVVF--VGGTLVLGTILF--------LVSQGLLSLQAKQEYCLKPECIEAAAAIL 67
Db     29 GAIVTLGVFYSIGKQLPLLTSLLHFSWDERTVVKRALRDSSLKSDICTTPSCVIAAARIL 88

Qy     68 SKVNLSVDPCDNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLEKSISRRR 127
Db     89 ENMDQSRNPCENFYQYACGGWLRHHVIPETNSRYSVFDILRDELEVILKGVLEDSTSQHR 148

Qy    128 DTEAIQKAKILYSSCMNEKAIEKADAKPLLHILRHSPFRWPVLESNIGPEGVWSER---K 184
Db    149 --PAVEKAKTLYRSCMNQSVIEKRDSEPLLSVLK-MVGGWPVAMDK------WNETMGLK 199

Qy    185 FSLLQTLATFRGQYSNSVFIRLYVSPDDKASNEHILKLDQATLSLAVREDYLDNSTEAKS 244
Db    200 WELERQLAVLNSQFNRRVLIDLFIWNDDQNSSRHVIYIDQPTLGMPSREYYFQEDNNHK- 258

Qy    245 YRDALYKFMVDTAVL------LGANSSRAEHDMKSVLRLEIKIAEIMIPHENRTS-EAMY 297
Db    259 VRKAYLEFMTSVATMLRKDQNLSKESAMVREEMAEVLELETHLANATVPQEKRHDVTALY 318

Qy    298 NKMNISELSAM--IPQFDWLGYIKKV---IDTRLYPHLKDISPSENVVVRVPQYFKDLFR 352
Db    319 HRMDLMELQERFGLKGFNWTLFIQNVLSSVEVELF-------PDEEVVVYGIPYLENLED 371

Qy    353 ILGSERKKTIANYLVWRMVYSRIPNLSRRFQYRWLEFSRVIQGTTTLLPQWDKCVNFIES 412
Db    372 IIDSYSARTMQNYLVWRLVLDRIGSLSQRFKEARVDYRKALYGTTVEEVRWRECVSYVNS 431

Qy    413 ALPYVVGKMFVDVYFQEDKKEMMEELVEGVRWAFIDMLEKENEWMDAGTKRKAKEKARAV 472
Db    432 NMESAVGSLYIKRAFSKDSKSTVRELIEKIRSVFVDNLDELN-WMDEESKKKAQEKAMNI 490

Qy    473 LAKVGYPEFIM--NDTHVNEDLKAIKFSEADYFGNVLQTRKYLAQSDFFWLRKAVPKTEW 530
Db    491 REQIGYPDYILEDNNKHLDEEYSSLTFYEDLYFENGLQNLKNNAQRSLKKLREKVDQNLW 550

Qy    531 FTNPTTVNAFYSASTNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNG 590
Db    551 IIGAAVVNAFYSPNRNQIVFPAGILQPPFF-SKDQPQSLNFGGIGMVIGHEITHGFDDNG 609

Qy    591 RKYDKNGNLDPWWSTESEEKFKEKTKCMINQYSNYYWKKA-GLNVKGKRTLGENIADNGG 649
Db    610 RNFDKNGNMLDWWSNFSARHFQQQSQCMIYQYGNFSWELADNQNVNGFSTLGENIADNGG 669

Qy    650 LREAFRAYRKWINDRRQGLEEPLLPGITFTNNQLFFLSYAHVRCNSYRPEAAREQVQIGA 709
Db    670 VRQAYKAYLRWLAD---GGKDQRLPGLNLTYAQLFFINYAQVWCGSYRPEFAVQSIKTDV 726

Qy    710 HSPPQFRVNGAISNSEEFQKAFNCPPNSTMNRGMDSCRLW 749
Db    727 HSPLKYRVLGSLQNLPGFSEAFHCPRGSPMH-PMKRCRIW 765
```

RESULT 5
AAB60562
ID AAB60562 standard; Protein; 753 AA.
XX
AC AAB60562;
XX
DT 27-APR-2001 (first entry)
XX
DE Human neprilysin-like membrane metallopeptidase SNEPb.
XX
KW Human; SNEPb; neprilysin-like membrane metallopeptidase;
KW splice variant; alternative splicing; zinc endopeptidase family;
KW neuropeptide; peptide hormone; processing; metabolism; vaccine;
KW drug screening; renal insufficiency; hepatic disease; ischaemia; pain;
KW hypertension; cancer; inflammation; cardiovascular disease;
KW neuronal disease; pancreatic disease; prostatic disease;
KW respiratory disease; gene therapy; nephrotropic; vasotropic; analgesic;
KW cerebroprotective; hypotensive; cytostatic; antiinflammatory;
KW cardiovascular; hepatotropic.
XX
OS Homo sapiens.
XX
PN EP1069188-A1.
XX
PD 17-JAN-2001.
XX
PF 15-JUL-1999; 99EP-0401767.
XX
PR 15-JUL-1999; 99EP-0401767.
XX
PA (SNFI) SANOFI-SYNTHELABO.
XX
PI Jagerschmidt A, Agnel M, Culouscou J;
XX
DR WPI; 2001-212582/22.
DR N-PSDB; AAF59660.
XX
PT New membrane-associated metallopeptidase SNEPa, SNEPb and SNEPc
PT polypeptides and polynucleotides, useful for treating e.g. acute and
PT chronic renal insufficiency, pain, stroke, cancer, inflammation, renal
PT and hepatic ischemia -
XX
PS Claim 11; Page 33-35; 72pp; English.
XX
CC The invention relates to the human SNEPa, SNEPb and SNEPc proteins, and
CC the cDNAs encoding them. SNEPa, SNEPb and SNEPc are neprilysin-like
CC membrane metallopeptidases and are the products of alternative splicing.
CC The substrate(s) for the SNEP proteins are not as yet known, although
CC the neprilysin family of zinc endopeptidases play key roles in the
CC processing and/or metabolism or neuropeptides and peptide hormones. SNEP
CC nucleotides may be used as hybridisation probes for cDNA and genomic
CC DNA; to isolate full-length cDNAs and genomic clones encoding SNEPa,
CC SNEPb or SNEPc; to isolate cDNA and genomic clones of SNEP homologues;
CC as research reagents and material for the discovery of treatments and
CC diagnostics for animal and human diseases; and for chromosome
CC identification. The SNEP proteins may be used as immunogens to
CC produce antibodies immunospecific for SNEPa, SNEPb or SNEPc. Such
CC antibodies are used to isolate or identify clones expressing the
CC protein, or to purify the proteins by affinity chromatography.
CC SNEP proteins may also be used in screening for compounds which modulate
CC SNEP endopeptidase activity, and to assess enzymatic cleavage of small
CC molecule substrates in cells, cell-free preparations, chemical libraries
CC and product mixtures. The SNEP proteins (as vaccine compositions),
CC SNEP nucleotides, and SNEP activators or inhibitors may used
CC to treat acute and chronic renal insufficiency, renal and hepatic
CC ischaemia, pain, stroke, hypertensive disease, cancer, inflammation, as
CC well as cardiovascular, neuronal, pancreatic, prostatic, renal,
CC respiratory or hepatic diseases. they may also be used in modulating
CC peptide activation and/or degradation in the brain or kidney or in
CC another organ, or to diagnose or treat any disorder related to abnormal
CC expression of SNEPa, SNEPb or SNEPc. The present sequence represents
CC SNEPb.
XX
SQ Sequence 753 AA;

Query Match 34.4%; Score 1362; DB 22; Length 753;
Best Local Similarity 38.6%; Pred. No. 6.6e-108;
Matches 295; Conservative 152; Mismatches 273; Indels 44; Gaps 18;

```
Qy      9 VETGKKANR-------GTRIALVVFVGGTLVLGTILFLVSQGLLSLQAKQEYCLKPECIE 61
          ||:  :| :       |  : |:: |   ||   :|:   :|:    |   | |  | |:
Db     11 VESAGRAGQKRPGFLEGGLLLLLLLVTAALVALGVLYADRRGIPEAQEVSEVCTTPGCVI 70

Qy     62 AAAAILSKVNLSVDPCDNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLEK 121
          ||| ||  :: : :|||:|::||| ||:  : |||    | ::  ||  ::: || :||
Db     71 AAARILQNMDPTTEPCDDFYQFACGGWLRRHVIPETNSRYSIFDVLRDELEVILKAVLEN 130

Qy    122 SISRRRDTEAIQKAKILYSSCMNEKAIEKADAKPLLHILRHSPFRWPVLESNIGPEGVWS 181
          | :  :|  |::||: || ||||:  |||  ::||| ||       |||          |:
Db    131 STA--KDRPAVEKARTLYRSCMNQSVIEKRGSQPLLDIL-EVVGGWPVAMDR------WN 181

Qy    182 ER---KFSLLQTLATFRGQYSNSVFIRLYVSPDDKASNEHILKLDQATLSLAVREDYLDN 238
          |    :: | : ||    |::  | | |::  ||: |: ||: :|| || :  || | :
Db    182 ETVGLEWELERQLALMNSQFNRRVLIDLFIWNDDQNSSRHIIYIDQPTLGMPSREYYFNG 241

Qy    239 STEAKSYRDALYKFMVDTAVLL--GANSSR----AEHDMKSVLRLEIKIAEIMIPHENRT 292
          :  |  |:|  :|||  | ||   ||  |     : ||  || || ::|:  :| | |
Db    242 GSNRK-VREAYLQFMVSVATLLREDANLPRDSCLVQEDMVQVLELETQLAKATVPQEERH 300

Qy    293 SE-AMYNKMNISELSAM--IPQFDWLGYIKKVIDTRLYPHLK-DISPSENVVVRVPQYFK 348
             |:|::| : || :   :  |||  :|: |: :     :|  : | | |||     | :
Db    301 DVIALYHRMGLEELQSQFGLKGFDWTLFIQTVLSS-----VKIKLLPDEEVVVYGIPYLQ 355

Qy    349 DLFRILGSERKKTIANYLVWRMVYSRIPNLSRRFQYRWLEFSRVIQGTTTLLPQWDKCVN 408
          :|  |: :   :|| |||||:|  || :||:||:   : : : : ||     :| :||
Db    356 NLENIIDTYSARTIQNYLVWRLVLDRIGSLSQRFKDTRVNYRKALFGTMVEEVRWRECVG 415

Qy    409 FIESALPYVVGKMFVDVYFQEDKKEMMEELVEGVRWAFIDMLEKENEWMDAGTKRKAKEK 468
          :: | :   || ::|.  |  | | |: ||:: ||  |:: |: |  |||  :|:||:||
Db    416 YVNSNMENAVGSLYVREAFPGDSKSMVRELIDKVRTVFVETLD-ELGWMDEESKKKAQEK 474

Qy    469 ARAVLAKVGYPEFIMNDTH--VNEDLKAIKFSEADYFGNVLQTRKYLAQSDFFWLRKAVP 526
          | ::  ::|:|::|: :|:  ::|:   : |||  || | ||  |  ||     ||: |
Db    475 AMSIREQIGHPDYILEETNRRLDEEYSNLNFSEDLYFENSLQNLKVGAQRSLRKLREKVD 534

Qy    527 KTEWFTNPTTVNAFYSASTNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGF 586
             |      |||||| : ||| |||| || |||   | |::|::| ||:::||| ||||
Db    535 PNLWIIGAAVVNAFYSPNRNQIVFPAGILQPPFF-SKEQPQALNFGGIGMVIGHEITHGF 593

Qy    587 DNNGRKYDKNGNLDPWWSTESEEKFKEKTKCMINQYSNYYWKKAG-LNVKGKRTLGENIA 645
          |:||| :|||||: ' |||  | : |:|:::||| || || |  |   || |  |||||||
Db    594 DDNGRNFDKNGNMMDWWSNFSTQHFREQSECMIYQYGNYSWDLADEQNVNGFNTLGENIA 653

Qy    646 DNGGLREAFRAYRKWINDRRQGLEEPLLPGITFTNNQLFFLSYAHVRCNSYRPEAAREQV 705
          ||||:|:|::|| ||:    :| ::  |||:  |: |||||:|| | | ||||| | : :
Db    654 DNGGVRQAYKAYLKWM---AEGGKDQQLPGLDLTHEQLFFINYAQVWCGSYRPEFAIQSI 710

Qy    706 QIGAHSPPQFRVNGAISNSEEFQKAFNCPPNSTMNRGMDSCRLW 749
          :  ||| ::|! |:: |   |   |:|   : |:   : ||:|
Db    711 KTDVHSPLKYRVLGSLQNLAAFADTFHCARGTPMH-PKERCRVW 753
```

RESULT 6
AAB83842
ID AAB83842 standard; Protein; 753 AA.
XX
AC AAB83842;
XX
DT 23-JUL-2001 (first entry)
XX
DE Amino acid sequence of a human metalloprotease enzyme IGS5.
XX
KW Metalloprotease; IGS5; infection; pain; cancer; diabetes; obesity;
KW anorexia; bulimia; asthma; Parkinson's disease; acute heart failure;

```
KW   hypotension; hypertension; urinary retention; osteoporosis;
KW   angina pectoris; myocardial infarction; stroke; ulcer; allergy;
KW   benign prostatic hypertrophy; migraine; psychotic disorder;
KW   neurological disorder; autism; multiple sclerosis; Alzheimer's disease;
KW   neurodegenerative disease; sleep disorder; epilepsy; kidney disease;
KW   cardiovascular disease; arteriosclerosis; cerebrovasospasm;
KW   subarachnoid hemorrhage; cerebral ischemia; cerebral infarction;
KW   peripheral vascular disease; Raynaud's disease; motility disorder;
KW   gastrointestinal disorder; gastric emptying; gastroparesis; diarrhoea;
KW   inflammation; chemotherapy induced injury; tumour invasion;
KW   immune disorder; arthritis; endotoxin shock; sepsis; diabetes mellitus;
KW   severe mental retardation; dyskinesia; Huntington's disease;
KW   Gilles de la Tourette's syndrome.
XX
OS   Homo sapiens.
XX
PN   WO200136610-A1.
XX
PD   25-MAY-2001.
XX
PF   17-NOV-2000; 2000WO-EP11532.
XX
PR   19-NOV-1999;   99EP-0203862.
PR   19-NOV-1999;   99NL-1013616.
PR   31-MAY-2000; 2000EP-0201937.
PR   31-MAY-2000; 2000NL-1015356.
XX
PA   (SOLV ) SOLVAY PHARM BV.
XX
PI   Deleersnijder W,  Wiegers R,  Weske M;
XX
DR   WPI; 2001-343815/36.
DR   N-PSDB; AAF89739.
XX
PT   New IGS5 polypeptides useful for treating infections, pain, cancer,
PT   diabetes, obesity, anorexia, bulimia, asthma, schizophrenia,
PT   hypertension, urinary retention and Parkinson's disease  -
XX
PS   Claim 3; Page 9-10; 115pp; English.
XX
CC   The present sequence represents a human metalloprotease enzyme designated
CC   IGS5. IGS5 polynucleotides and polypeptides are useful for treating
CC   infections, pain, cancer, diabetes, obesity, anorexia, bulimia, asthma,
CC   Parkinson's disease, acute heart failure, hypotension, hypertension,
CC   urinary retention, osteoporosis, angina pectoris, myocardial infarction,
CC   stroke, ulcers, allergies, benign prostatic hypertrophy, migraine,
CC   psychotic and neurological disorders, autism, multiple sclerosis,
CC   Alzheimer's disease, and other neurodegenerative diseases, sleep
CC   disorder, epilepsy, cardiovascular diseases, arteriosclerosis,
CC   cerebrovasospasm, subarachnoid hemorrhage, cerebral ischemia, cerebral
CC   infarction, peripheral vascular disease, Raynaud's disease, kidney
CC   diseases, gastrointestinal disorders, motility disorders and conditions
CC   of delayed gastric emptying, post-operative or diabetic gastroparesis,
CC   diarrhoea, inflammations, chemotherapy induced injury, tumour invasion,
CC   immune disorders, arthritis, endotoxin shock, sepsis, complications of
CC   diabetes mellitus, and severe mental retardation and dyskinesias, such
CC   as Huntington's disease or Gilles de la Tourette's syndrome.
XX
SQ   Sequence   753 AA;

  Query Match             34.2%;  Score 1352;  DB 22;  Length 753;
  Best Local Similarity   38.4%;  Pred. No. 4.8e-107;
  Matches  293;  Conservative  153;  Mismatches  274;  Indels   44;  Gaps   18;

Qy       9 VETGKKANR-------GTRIALVVFVGGTLVLGTILFLVSQGLLSLQAKQEYCLKPECIE 61
Db      11 VESAGRAGQKRPGFLEGGLLLLLLLVTAALVALGVLYADRRGIPEAQEVSEVCTTPGCVI 70

Qy      62 AAAAILSKVNLSVDPCDNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLEK 121
Db      71 AAARILQNMDPTTEPCDDFYQFACGGWLRRHVIPETNSRYSIFDVLRDELEVILKAVLEN 130

Qy     122 SISRRRDTEAIQKAKILYSSCMNEKAIEKADAKPLLHILRHSPFRWPVLESNIGPEGVWS 181
Db     131 STA--KDRPAVEKARTLYRSCMNQSVIEKRGSQPLLDIL-EVVGGWPVAMDR------WN 181

Qy     182 ER---KFSLLQTLATFRGQYSNSVFIRLYVSPDDKASNEHILKLDQATLSLAVREDYLDN 238
Db     182 ETVGLEWELERQLALMNSQFNRRVLIDLFIWNDDQNSSRHIIYIDQPTLGMPSREYYFNG 241

Qy     239 STEAKSYRDALYKFMVDTAVLL--GANSSR----AEHDMKSVLRLEIKIAEIMIPHENRT 292
Db     242 GSNRK-VREAYLQFMVSVATLLREDANLPRDSCLVQEDMMQVLELETQLAKATVPQEERH 300

Qy     293 SE-AMYNKMNISELSAM--IPQFDWLGYIKKVIDTRLYPHLK-DISPSENVVVRVPQYFK 348
Db     301 DVIALYHRMGLEELQSQFGLKGFNWTLFIQTVLSS-----VKIKLLPDEEVVVYGIPYLQ 355

Qy     349 DLFRILGSERKKTIANYLVWRMVYSRIPNLSRRFQYRWLEFSRVIQGTTTLLPQWDKCVN 408
Db     356 NLENIIDTYSARTIQNYLVWRLVLDRIGSLSQRFKDTRVNYRKALFGTMVEEVRWRECVG 415

Qy     409 FIESALPYVVGKMFVDVYFQEDKKEMMEELVEGVRWAFIDMLEKENEWMDAGTKRKAKEK 468
Db     416 YVNSNMENAVGSLYVREAFPGDSKSMVRELIDKVRTVFVETLD-ELGWMDEESKKKAQEK 474

Qy     469 ARAVLAKVGYPEFIMNDTH--VNEDLKAIKFSEADYFGNVLQTRKYLAQSDFFWLRKAVP 526
Db     475 AMSIREQIGHPDYILEEMNRRLDEEYSNLNFSEDLYFENSLQNLKVGAQRSLRKLREKVD 534

Qy     527 KTEWFTNPTTVNAFYSASTNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGF 586
Db     535 PNLWIIGAAVVNAFYSPNRNQIVFPAGILQPPFF-SKEQPQALNFGGIGMVIGHEITHGF 593

Qy     587 DNNGRKYDKNGNLDPWWSTESEEKFKEKTKCMINQYSNYYWKKAG-LNVKGKRTLGENIA 645
Db     594 DDNGRNFDKNGNMMDWWSNFSTQHFREQSECMIYQYGNYSWDLADEQNVNGFNTLGENIA 653

Qy     646 DNGGLREAFRAYRKWINDRRQGLEEPLLPGITFTNNQLFFLSYAHVRCNSYRPEAAREQV 705
Db     654 DNGGVRQAYKAYLKWM---AEGGKDQQLPGLDLTHEQLFFINYAQVWCGSYRPEFAIQSI 710

Qy     706 QIGAHSPPQFRVNGAISNSEEFQKAFNCPPNSTMNRGMDSCRLW 749
Db     711 KTDVHSPLKYRVLGSLQNLAAFADTFHCARGTPMH-PKERCRVW 753


RESULT 7
AAY44177
ID   AAY44177 standard; Protein; 774 AA.
XX
AC   AAY44177;
XX
DT   01-FEB-2000  (first entry)
XX
DE   Rat membrane metalloprotease NEPII protein.
XX
KW   Rat; membrane metalloprotease; neprilysine II; NEPII; inactivation;
KW   neuron; hormone; peptide messenger; inhibitor; detection; disorder;
KW   cardiovascular disease; neurodegenerative disease; growth disorder;
KW   hypothalamic-hypophyseal axis; endocrine disorder.
XX
OS   Rattus rattus.
XX
PN   FR2777291-A1.
XX
PD   15-OCT-1999.
XX
PF   08-APR-1998;   98FR-0004389.
XX
PR   08-APR-1998;   98FR-0004389.
XX
PA   (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
XX
PI   Ouimet T,  Gros C,  Haret C,  Bonhomme MC,  Facchinetti P;
PI   Schwartz JC;
```

XX
DR WPI; 1999-593429/51.
DR N-PSDB; AAZ28810.
XX
PT New membrane metalloprotease NEP II, involved in proteolysis of
PT neuronal and hormonal peptides, used to screen for inhibitors,
PT potentially useful for treating e.g. cardiovascular disease -
XX
PS Claim 1; Page 12-16; 29pp; French.
XX
CC This sequence represents the rat membrane metalloprotease designated
CC neprilysine II (NEPII), which is involved in (in)activation of neuronal
CC and hormonal peptide messengers. NEPII is used to screen for specific
CC substrates (used to detect NEPII in cells and tissues) or inhibitors,
CC which can also be used to detect NEPII or for treatment of disorders
CC related to peptidergic signalling in which NEPII in involved, e.g.
CC cardiovascular or neurodegenerative diseases; growth disorders of
CC endocrine origin; disturbances of the hypothalamic-hypophyseal axis
CC or endocrine disorders.
XX
SQ Sequence 774 AA;

Query Match 34.1%; Score 1351; DB 20; Length 774;
Best Local Similarity 38.2%; Pred. No. 6.1e-107;
Matches 289; Conservative 156; Mismatches 266; Indels 46; Gaps 18;

```
Qy     18 GTRIALVVF--VGGTL-VLGTILF-------LVSQGLLSLQAKQEYCLKPECIEAAAAIL 67
          |  : | ||  :|  | :| ::|         :| : |     | : |  | |: ||| ||
Db     39 GAIVTLGVFYSIGKQLPLLNSLLHVSRHERTVVKRVLRDSSQKSDICTTPSCVIAAARIL 98

Qy     68 SKVNLSVDPCDNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLEKSISRRR 127
            :: |  |||||:::|| ||: :: |||    | |:  ||  ::: || :|| |  : |
Db     99 QNMDQSKKPCDNFYQYACGGWLRHHVIPETNSRYSVFDILRDELEVILKGVLEDSSVQHR 158

Qy    128 DTEAIQKAKILYSSCMNEKAIEKADAKPLLHILRHSPFRWPVLESNIGPEGVWSER---K 184
             |::||| || ||||:  ||| |::|||::|      |||          |:|    |
Db    159 --PAVEKAKTLYRSCMNQSVIEKRDSEPLLNVL-DMIGGWPVAMDK------WNETMGPK 209

Qy    185 FSLLQTLATFRGQYSNSVFIRLYVSPDDKASNEHILKLDQATLSLAVREDYLDNSTEAKS 244
          : | : ||    |::  | | |::  ||: |: |:: :|| || :  || |     ::
Db    210 WELERQLAVLNSQFNRRVLIDLFIWNDDQNSSRHVIYIDQPTLGMPSREYYF--KEDSHR 267

Qy    245 YRDALYKFMVDTAVL------LGANSSRAEHDMKSVLRLEIKIAEIMIPHENRTS-EAMY 297
            |:|  :||   | :       |   :   : :|  || ||  :|   :| | |    |:|
Db    268 VREAYLQFMTSVATMLRRDLNLPGETDLVQEEMAQVLHLETHLANATVPQEKRHDVTALY 327

Qy    298 NKMNISELSAM--IPQFDWLGYIKKVIDTRLYPHLKDISPSENVVVRVPQYFKDLFRILG 355
          ::| : ||     :  |:|  :|: |: :       :: |:| |||    | ::|  |:
Db    328 HRMGLEELQERFGLKGFNWTLFIQNVLSSVQV----ELLPNEEVVVYGIPYLENLEEIID 383

Qy    356 SERKKTIANYLVWRMVYSRIPNLSRRFQYRWLEFSRVIQGTTTLLPQWDKCVNFIESALP 415
             :|: ||||||:|  || :||:||:   ::: : : |||    :| :||::: | :
Db    384 VFPAQTLQNYLVWRLVLDRIGSLSQRFKEARVDYRKALYGTTMEEVRWRECVSYVNSNME 443

Qy    416 YVVGKMFVDVYFQEDKKEMMEELVEGVRWAFIDMLEKENEWMDAGTKRKAKEKARAVLAK 475
             || :::   | :| | :: ||:| :|  |:| |:: | |||  :|:||:|||  :  :
Db    444 SAVGSLYIKRAFSKDSKSIVSELIEKIRSVFVDNLDELN-WMDEESKKKAQEKALNIREQ 502

Qy    476 VGYPEFIM--NDTHVNEDLKAIKFSEADYFGNVLQTRKYLAQSDFFWLRKAVPKTEWFTN 533
          :|||::|:  |: |::|:  :: ||| || | ||  |  ||     ||: | :  |
Db    503 IGYPDYILEDNNRHLDEEYSSLTFSEDLYFENGLQNLKNNAQRSLKKLREKVDQNLWIIG 562

Qy    534 PTTVNAFYSASTNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNGRKY 593
             |||||| : | | |||| || |||   : |::|::| ||:::||| |||||:||| :
Db    563 AAVVNAFYSPNRNLIVFPAGILQPPFF-SKDQPQALNFGGIGMVIGHEITHGFDDNGRNF 621

Qy    594 DKNGNLDPWWSTESEEKFKEKTKCMINQYSNYYWKKA-GLNVKGKRTLGENIADNGGLRE 652
          |||||:  |||  |   |:::::|||  ||||: |: |   || |  ||||||||||:|:
Db    622 DKNGNMLDWWSNFSARHFRQQSQCMIYQYSNFSWELADNQNVNGFSTLGENIADNGGVRQ 681

Qy    653 AFRAYRKWINDRRQGLEEPLLPGITFTNNQLFFLSYAHVRCNSYRPEAAREQVQIGAHSP 712
             |::|| :|:    :|  :  |||:  |  ||||::|| | | ||||| | : ::   |||
Db    682 AYKAYLQWL---AEGGRDQRLPGLNLTYAQLFFINYAQVWCGSYRPEFAIQSIKTDVHSP 738

Qy    713 PQFRVNGAISNSEEFQKAFNCPPNSTMNRGMDSCRLW 749
             ::|| |:: |   | :||:||  | |:  |: ||:|
Db    739 LKYRVLGSLQNLPGFSEAFHCPRGSPMH-PMNRCRIW 774
```

RESULT 8
AAB60561
ID AAB60561 standard; Protein; 779 AA.
XX
AC AAB60561;
XX
DT 27-APR-2001 (first entry)
XX
DE Human neprilysin-like membrane metallopeptidase SNEPa.
XX
KW Human; SNEPa; neprilysin-like membrane metallopeptidase;
KW splice variant; alternative splicing; zinc endopeptidase family;
KW neuropeptide; peptide hormone; processing; metabolism; vaccine;
KW drug screening; renal insufficiency; hepatic disease; ischaemia; pain;
KW hypertension; cancer; inflammation; cardiovascular disease;
KW neuronal disease; pancreatic disease; prostatic disease;
KW respiratory disease; gene therapy; nephrotropic; vasotropic; analgesic;
KW cerebroprotective; hypotensive; cytostatic; antiinflammatory;
KW cardiovascular; hepatotropic.
XX
OS Homo sapiens.
XX
PN EP1069188-A1.
XX
PD 17-JAN-2001.
XX
PF 15-JUL-1999; 99EP-0401767.
XX
PR 15-JUL-1999; 99EP-0401767.
XX
PA (SNFI) SANOFI-SYNTHELABO.
XX
PI Jagerschmidt A, Agnel M, Culouscou J;
XX
DR WPI; 2001-212582/22.
DR N-PSDB; AAF59659.
XX
PT New membrane-associated metallopeptidase SNEPa, SNEPb and SNEPc
PT polypeptides and polynucleotides, useful for treating e.g. acute and
PT chronic renal insufficiency, pain, stroke, cancer, inflammation, renal
PT and hepatic ischemia -
XX
PS Claim 11; Page 28-30; 72pp; English.
XX
CC The invention relates to the human SNEPa, SNEPb and SNEPc proteins, and
CC the cDNAs encoding them. SNEPa, SNEPb and SNEPc are neprilysin-like
CC membrane metallopeptidases and are the products of alternative splicing.
CC The substrate(s) for the SNEP proteins are not as yet known, although
CC the neprilysin family of zinc endopeptidases play key roles in the
CC processing and/or metabolism or neuropeptides and peptide hormones. SNEP
CC nucleotides may be used as hybridisation probes for cDNA and genomic
CC DNA; to isolate full-length cDNAs and genomic clones encoding SNEPa,
CC SNEPb or SNEPc; to isolate cDNA and genomic clones of SNEP homologues;
CC as research reagents and material for the discovery of treatments and
CC diagnostics for animal and human diseases; and for chromosome
CC identification. The SNEP proteins may be used as immunogens to
CC produce antibodies immunospecific for SNEPa, SNEPb or SNEPc. Such
CC antibodies are used to isolate or identify clones expressing the
CC protein, or to purify the proteins by affinity chromatography.
CC SNEP proteins may also be used in screening for compounds which modulate
CC SNEP endopeptidase activity, and to assess enzymatic cleavage of small
CC molecule substrates in cells, cell-free preparations, chemical libraries
CC and product mixtures. The SNEP proteins (as vaccine compositions),
CC SNEP nucleotides, and SNEP activators or inhibitors may used
CC to treat acute and chronic renal insufficiency, renal and hepatic
CC ischaemia, pain, stroke, hypertensive disease, cancer, inflammation, as
CC well as cardiovascular, neuronal, pancreatic, prostatic, renal,

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CC   respiratory or hepatic diseases. they may also be used in modulating
CC   peptide activation and/or degradation in the brain or kidney or in
CC   another organ, or to diagnose or treat any disorder related to abnormal
CC   expression of SNEPa, SNEPb or SNEPc. The present sequence represents
CC   SNEPa.
XX
SQ   Sequence   779 AA;

  Query Match             33.9%;  Score 1343.5;  DB 22;  Length 779;
  Best Local Similarity   39.5%;  Pred. No. 2.7e-106;
  Matches  286;  Conservative  144;  Mismatches  257;  Indels   37;  Gaps   17;

Qy      42 QGLLSLQAKQEYCLKPECIEAAAAILSKVNLSVDPCDNFFRFACDGWISNNPIPEDMPSY 101
           :|:   |   | |  | |: ||| ||  :: : :|||:|::||| ||:  : |||    |
Db      77 RGIPEAQEVSEVCTTPGCVIAAARILQNMDPTTEPCDDFYQFACGGWLRRHVIPETNSRY 136

Qy     102 GVYPWLRHNVDLKLKELLEKSISRRRDTEAIQKAKILYSSCMNEKAIEKADAKPLLHILR 161
           ::  ||  ::: || :|| | :  :|  |::||: || ||||:  |||  ::||| ||
Db     137 SIFDVLRDELEVILKAVLENSTA--KDRPAVEKARTLYRSCMNQSVIEKRGSQPLLDIL- 193

Qy     162 HSPFRWPVLESNIGPEGVWSER---KFSLLQTLATFRGQYSNSVFIRLYVSPDDKASNEH 218
           |||             |:|    :: | : ||    |::  | | |::  ||: |: |
Db     194 EVVGGWPVAMDR------WNETVGLEWELERQLALMNSQFNRRVLIDLFIWNDDQNSSRH 247

Qy     219 ILKLDQATLSLAVREDYLDNSTEAKSYRDALYKFMVDTAVLL--GANSSR----AEHDMK 272
           |: :|| || :  || | :  :  |  |:|  :|||  | ||  || |     : ||
Db     248 IIYIDQPTLGMPSREYYFNGGSNRK-VREAYLQFMVSVATLLREDANLPRDSCLVQEDMV 306

Qy     273 SVLRLEIKIAEIMIPHENRTSE-AMYNKMNISELSAM--IPQFDWLGYIKKVIDTRLYPH 329
           || || ::|:  :| | |    |:|::| : || :   :  |||  :|: |: :
Db     307 QVLELETQLAKATVPQEERHDVIALYHRMGLEELQSQFGLKGFDWTLFIQTVLSS----- 361

Qy     330 LK-DISPSENVVVRVPQYFKDLFRILGSERKKTIANYLVWRMVYSRIPNLSRRFQYRWLE 388
           :|  : | | |||    | ::|  |: :   :|| ||||||:|  || :||:||:   :
Db     362 VKIKLLPDEEVVVYGIPYLQNLENIIDTYSARTIQNYLVWRLVLDRIGSLSQRFKDTRVN 421

Qy     389 FSRVIQGTTTLLPQWDKCVNFIESALPYVVGKMFVDVYFQEDKKEMMEELVEGVRWAFID 448
           : : : ||     :| :|| :: | :   || ::|   |  | | |: ||:: ||  |::
Db     422 YRKALFGTMVEEVRWRECVGYVNSNMENAVGSLYVREAFPGDSKSMVRELIDKVRTVFVE 481

Qy     449 MLEKENEWMDAGTKRKAKEKARAVLAKVGYPEFIMNDTH--VNEDLKAIKFSEADYFGNV 506
           |: |  |||  :|:||:||| ::  ::|:|::|: :|:  ::|:   : |||  || |
Db     482 TLD-ELGWMDEESKKKAQEKAMSIREQIGHPDYILEETNRRLDEEYSNLNFSEDLYFENS 540

Qy     507 LQTRKYLAQSDFFWLRKAVPKTEWFTNPTTVNAFYSASTNQIRFPAGELQKPFFWGTEYP 566
           ||  |  ||    ||: |    |      ||||||  : ||| |||| || |||   | |
Db     541 LQNLKVGAQRSLRKLREKVDPNLWIIGAAVVNAFYSPNRNQIVFPAGILQPPFF-SKEQP 599

Qy     567 RSLSYGAIGVIVGHEFTHGFDNNGRKYDKNGNLDPWWSTESEEKFKEKTKCMINQYSNYY 626
           ::|::| ||:::||| |||||:||| :|||||:  |||  | : |:|:::||| || ||
Db     600 QALNFGGIGMVIGHEITHGFDDNGRNFDKNGNMMDWWSNFSTQHFREQSECMIYQYGNYS 659

Qy     627 WKKAG-LNVKGKRTLGENIADNGGLREAFRAYRKWINDRRQGLEEPLLPGITFTNNQLFF 685
           |  |   || |  |||||||||||:|:|::|| ||:    :| ::  |||:  |: ||||
Db     660 WDLADEQNVNGFNTLGENIADNGGVRQAYKAYLKWM---AEGGKDQQLPGLDLTHEQLFF 716

Qy     686 LSYAHVRCNSYRPEAAREQVQIGAHSPPQFRVNGAISNSEEFQKAFNCPPNSTMNRGMDS 745
           ::|| | | ||||| | : ::   ||| ::|| |:: |   |   |:|   : |:   :
Db     717 INYAQVWCGSYRPEFAIQSIKTDVHSPLKYRVLGSLQNLAAFADTFHCARGTPMH-PKER 775

Qy     746 CRLW 749
           ||:|
Db     776 CRVW 779


RESULT 9
AAB83841
ID   AAB83841 standard; Protein; 779 AA.
XX
AC   AAB83841;
XX
DT   23-JUL-2001  (first entry)
XX
DE   Amino acid sequence of a human metalloprotease enzyme IGS5.
XX
KW   Metalloprotease; IGS5; infection; pain; cancer; diabetes; obesity;
KW   anorexia; bulimia; asthma; Parkinson's disease; acute heart failure;
KW   hypotension; hypertension; urinary retention; osteoporosis;
KW   angina pectoris; myocardial infarction; stroke; ulcer; allergy;
KW   benign prostatic hypertrophy; migraine; psychotic disorder;
KW   neurological disorder; autism; multiple sclerosis; Alzheimer's disease;
KW   neurodegenerative disease; sleep disorder; epilepsy; kidney disease;
KW   cardiovascular disease; arteriosclerosis; cerebrovasospasm;
KW   subarachnoid hemorrhage; cerebral ischemia; cerebral infarction;
KW   peripheral vascular disease; Raynaud's disease; motility disorder;
KW   gastrointestinal disorder; gastric emptying; gastroparesis; diarrhoea;
KW   inflammation; chemotherapy induced injury; tumour invasion;
KW   immune disorder; arthritis; endotoxin shock; sepsis; diabetes mellitus;
KW   severe mental retardation; dyskinesia; Huntington's disease;
KW   Gilles de la Tourette's syndrome.
XX
OS   Homo sapiens.
XX
PN   WO200136610-A1.
XX
PD   25-MAY-2001.
XX
PF   17-NOV-2000; 2000WO-EP11532.
XX
PR   19-NOV-1999;   99EP-0203862.
PR   19-NOV-1999;   99NL-1013616.
PR   31-MAY-2000; 2000EP-0201937.
PR   31-MAY-2000; 2000NL-1015356.
XX
PA   (SOLV ) SOLVAY PHARM BV.
XX
PI   Deleersnijder W,  Wiegers R,  Weske M;
XX
DR   WPI; 2001-343815/36.
DR   N-PSDB; AAF89738.
XX
PT   New IGS5 polypeptides useful for treating infections, pain, cancer,
PT   diabetes, obesity, anorexia, bulimia, asthma, schizophrenia,
PT   hypertension, urinary retention and Parkinson's disease -
XX
PS   Claim 3; Page 8; 115pp; English.
XX
CC   The present sequence represents a human metalloprotease enzyme designated
CC   IGS5. IGS5 polynucleotides and polypeptides are useful for treating
CC   infections, pain, cancer, diabetes, obesity, anorexia, bulimia, asthma,
CC   Parkinson's disease, acute heart failure, hypotension, hypertension,
CC   urinary retention, osteoporosis, angina pectoris, myocardial infarction,
CC   stroke, ulcers, allergies, benign prostatic hypertrophy, migraine,
CC   psychotic and neurological disorders, autism, multiple sclerosis,
CC   Alzheimer's disease, and other neurodegenerative diseases, sleep
CC   disorder, epilepsy, cardiovascular diseases, arteriosclerosis,
CC   cerebrovasospasm, subarachnoid hemorrhage, cerebral ischemia, cerebral
CC   infarction, peripheral vascular disease, Raynaud's disease, kidney
CC   diseases, gastrointestinal disorders, motility disorders and conditions
CC   of delayed gastric emptying, post-operative or diabetic gastroparesis,
CC   diarrhoea, inflammations, chemotherapy induced injury, tumour invasion,
CC   immune disorders, arthritis, endotoxin shock, sepsis, complications of
CC   diabetes mellitus, and severe mental retardation and dyskinesias, such
CC   as Huntington's disease or Gilles de la Tourette's syndrome.
XX
SQ   Sequence   779 AA;

  Query Match             33.7%;  Score 1333.5;  DB 22;  Length 779;
  Best Local Similarity   39.2%;  Pred. No. 2e-105;
  Matches  284;  Conservative  145;  Mismatches  258;  Indels   37;  Gaps   17;

Qy      42 QGLLSLQAKQEYCLKPECIEAAAAILSKVNLSVDPCDNFFRFACDGWISNNPIPEDMPSY 101
           :|:   |   | |  | |: ||| ||  :: : :|||:|::||| ||:  : |||    |
Db      77 RGIPEAQEVSEVCTTPGCVIAAARILQNMDPTTEPCDDFYQFACGGWLRRHVIPETNSRY 136

Qy     102 GVYPWLRHNVDLKLKELLEKSISRRRDTEAIQKAKILYSSCMNEKAIEKADAKPLLHILR 161
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Db    137 SIFDVLRDELEVILKAVLENSTA--KDRPAVEKARTLYRSCMNQSVIEKRGSQPLLDIL- 193

Qy    162 HSPFRWPVLESNIGPEGVWSER---KFSLLQTLATFRGQYSNSVFIRLYVSPDDKASNEH 218

Db    194 EVVGGWPVAMDR------WNETVGLEWELERQLALMNSQFNRRVLIDLFIWNDDQNSSRH 247

Qy    219 ILKLDQATLSLAVREDYLDNSTEAKSYRDALYKFMVDTAVLL--GANSSR----AEHDMK 272

Db    248 IIYIDQPTLGMPSREYYFNGGSNRK-VREAYLQFMVSVATLLREDANLPRDSCLVQEDMM 306

Qy    273 SVLRLEIKIAEIMIPHENRTSE-AMYNKMNISELSAM--IPQFDWLGYIKKVIDTRLYPH 329

Db    307 QVLELETQLAKATVPQEERHDVIALYHRMGLEELQSQFGLKGFNWTLFIQTVLSS----- 361

Qy    330 LK-DISPSENVVVRVPQYFKDLFRILGSERKKTIANYLVWRMVYSRIPNLSRRFQYRWLE 388

Db    362 VKIKLLPDEEVVVYGIPYLQNLENIIDTYSARTIQNYLVWRLVLDRIGSLSQRFKDTRVN 421

Qy    389 FSRVIQGTTTLLPQWDKCVNFIESALPYVVGKMFVDVYFQEDKKEMMEELVEGVRWAFID 448

Db    422 YRKALFGTMVEEVRWRECVGYVNSNMENAVGSLYVREAFPGDSKSMVRELIDKVRTVFVE 481

Qy    449 MLEKENEWMDAGTKRKAKEKARAVLAKVGYPEFIMNDTH--VNEDLKAIKFSEADYFGNV 506

Db    482 TLD-ELGWMDEESKKKAQEKAMSIREQIGHPDYILEEMNRRLDEEYSNLNFSEDLYFENS 540

Qy    507 LQTRKYLAQSDFFWLRKAVPKTEWFTNPTTVNAFYSASTNQIRFPAGELQKPFFWGTEYP 566

Db    541 LQNLKVGAQRSLRKLREKVDPNLWIIGAAVVNAFYSPNRNQIVFPAGILQPPFF-SKEQP 599

Qy    567 RSLSYGAIGVIVGHEFTHGFDNNGRKYDKNGNLDPWWSTESEEKFKEKTKCMINQYSNYY 626

Db    600 QALNFGGIGMVIGHEITHGFDDNGRNFDKNGNMMDWWSNFSTQHFREQSECMIYQYGNYS 659

Qy    627 WKKAG-LNVKGKRTLGENIADNGGLREAFRAYRKWINDRRQGLEEPLLPGITFTNNQLFF 685

Db    660 WDLADEQNVNGFNTLGENIADNGGVRQAYKAYLKWM---AEGGKDQQLPGLDLTHEQLFF 716

Qy    686 LSYAHVRCNSYRPEAAREQVQIGAHSPPQFRVNGAISNSEEFQKAFNCPPNSTMNRGMDS 745

Db    717 INYAQVWCGSYRPEFAIQSIKTDVHSPLKYRVLGSLQNLAAFADTFHCARGTPMH-PKER 775

Qy    746 CRLW 749

Db    776 CRVW 779
```

```
RESULT 10
AAB08131
ID   AAB08131 standard; Protein; 770 AA.
XX
AC   AAB08131;
XX
DT   04-DEC-2000  (first entry)
XX
DE   A human neutral endopeptidase metallopeptidase-like enzyme NL-2.
XX
KW   Neprilysin; neutral endopeptidase metallopeptidase-like enzyme;
KW   NEP-like enzyme; protein production; protein secretion;
KW   neurological disease; Alzheimer's disease; pain; psychiatric disorder;
KW   fertility; bone disease; abnormal phosphate metabolism.
XX
OS   Homo sapiens.
XX
PN   WO200047750-A2.
XX
PD   17-AUG-2000.
XX
PF   11-FEB-2000; 2000WO-CA00147.
XX
PR   11-FEB-1999;   99CA-2260376.
XX
PA   (UYMO-) UNIV MONTREAL.
XX
PI   Desgroseillers L,  Boileau G;
XX
DR   WPI; 2000-549148/50.
DR   N-PSDB; AAA63764.
XX
PT   Novel neutral endopeptidase-like metallopeptidase polypeptides and
PT   polynucleotides, used to screen for related sequences and enzyme
PT   inhibitors, used for the treatment of NL-3 related bone disorders -
XX
PS   Claim 3; Fig 4; 59pp; English.
XX
CC   The present sequence represents a human neutral endopeptidase
CC   metallopeptidase-like enzyme, designated NL-2. The specification
CC   also describes NL-1 and NL-3. The NL enzymes are used to test for
CC   specific inhibitors. The N-terminal region of the enzymes can be used
CC   to promote production and secretion of foreign proteins and active
CC   biopeptides, using chimeric constructs containing the foreign protein
CC   downstream from and in phase with the N-terminal region. The NL enzymes
CC   are have been localised to the brain, and may be useful in the
CC   treatment of neurological diseases such as Alzheimer's disease, pain,
CC   and psychiatric disorders. NL enzymes have also been localised to the
CC   testis and ovaries, and may be used to control fertility. They have
CC   also been localised to bones, and may be used to treat bone diseases,
CC   and abnormal phosphate metabolisms related to improper peptide
CC   processing by the NL-3 enzyme.
XX
SQ   Sequence   770 AA;
```

Query Match 33.7%; Score 1332.5; DB 21; Length 770;
Best Local Similarity 39.2%; Pred. No. 2.4e-105;
Matches 284; Conservative 145; Mismatches 258; Indels 37; Gaps 17;

```
Qy     42 QGLLSLQAKQEYCLKPECIEAAAAILSKVNLSVDPCDNFFRFACDGWISNNPIPEDMPSY 101

Db     68 RGIPEAQEVSEVCTTPGCVIAAARILQNMDPTTEPCDDFYQFACGGWLRRHVIPETNSRY 127

Qy    102 GVYPWLRHNVDLKLKELLEKSISRRRDTEAIQKAKILYSSCMNEKAIEKADAKPLLHILR 161

Db    128 SIFDVLRDELEVILKAVLENSTA--KDRPAVEKARTLYRSCMNQSVIEKRGSQPLLDIL- 184

Qy    162 HSPFRWPVLESNIGPEGVWSER---KFSLLQTLATFRGQYSNSVFIRLYVSPDDKASNEH 218

Db    185 EVVGGWPVAMDR------WNETVGLEWELERQLALMNSQFNRRVLIDLFIWNDDQNSSRH 238

Qy    219 ILKLDQATLSLAVREDYLDNSTEAKSYRDALYKFMVDTAVLL--GANSSR----AEHDMK 272

Db    239 IIYIDQPTLGMPSREYYFNGGSNRK-VREAYLQFMVSVATLLREDANLPRDSCLVQEDMV 297

Qy    273 SVLRLEIKIAEIMIPHENRTSE-AMYNKMNISELSAM--IPQFDWLGYIKKVIDTRLYPH 329

Db    298 QVLELETQLAKATVPQEERHDVIALYHRMGLEELQSQFGLKGFNWTLFIQTVLSS----- 352

Qy    330 LK-DISPSENVVVRVPQYFKDLFRILGSERKKTIANYLVWRMVYSRIPNLSRRFQYRWLE 388

Db    353 VKIKLLPDEEVVVYGIPYLQNLENIIDTYSARTIQNYLVWRLVLDRIGSLSQRFKDTRVN 412

Qy    389 FSRVIQGTTTLLPQWDKCVNFIESALPYVVGKMFVDVYFQEDKKEMMEELVEGVRWAFID 448

Db    413 YRKALFGTMVEEVRWRECVGYVNSNMENAVGSLYVREAFPGDSKSMVRELIDKVRTVFVE 472

Qy    449 MLEKENEWMDAGTKRKAKEKARAVLAKVGYPEFIMNDTH--VNEDLKAIKFSEADYFGNV 506

Db    473 TLD-ELGWMDEESKKKAQEKAMSIREQIGHPDYILEEMNRRLDEEYSNLNFSEDLYFENS 531

Qy    507 LQTRKYLAQSDFFWLRKAVPKTEWFTNPTTVNAFYSASTNQIRFPAGELQKPFFWGTEYP 566

Db    532 LQNLKVGAQRSLRKLREKVDPNLWIIGAAVVNAFYSPNRNQIVFPAGILQPPFF-SKEQP 590

Qy    567 RSLSYGAIGVIVGHEFTHGFDNNGRKYDKNGNLDPWWSTESEEKFKEKTKCMINQYSNYY 626

Db    591 QALNFGGIGMVIGHEITHGFDDNGRNFDKNGNMMDWWSNFSTQHFREQSECMIYQYGNYS 650
```

```
Qy     627 WKKAG-LNVKGKRTLGENIADNGGLREAFRAYRKWINDRRQGLEEPLLPGITFTNNQLFF 685
           |  |   || |  ||||||||||||:|:|::|| ||:    :| ::  |||:  |: ||||
Db     651 WDLADEQNVNGFNTLGENIADNGGVRQAYKAYLKWM---AEGGKDQQLPGLDLTHEQLFF 707

Qy     686 LSYAHVRCNSYRPEAAREQVQIGAHSPPQFRVNGAISNSEEFQKAFNCPPNSTMNRGMDS 745
           ::|| | | ||||| | : ::   ||| ::|| |:: |   |   |:|   : |:   :
Db     708 INYAQVWCGSYRPEFAIQSIKTDVHSPLKYRVLGSLQNLAAFADTFHCARGTPMH-PKER 766

Qy     746 CRLW 749
           ||:|
Db     767 CRVW 770
```

RESULT 11
ABB79521
ID ABB79521 standard; Protein; 779 AA.
XX
AC ABB79521;
XX
DT 23-SEP-2002 (first entry)
XX
DE Human SEP endopeptidase.
XX
KW SEP; endopeptidase; enzyme; human; neuropeptide Y1; receptor;
KW male sexual dysfunction; male erectile dysfunction; obesity;
KW anorexia; bulimia; vasotropic; anorectic; therapy; inhibitor.
XX
OS Homo sapiens.
XX
PN WO200247670-A1.
XX
PD 20-JUN-2002.
XX
PF 10-DEC-2001; 2001WO-IB02399.
XX
PR 15-DEC-2000; 2000GB-0030647.
PR 06-APR-2001; 2001GB-0008730.
PR 23-APR-2001; 2001GB-0009910.
PR 04-MAY-2001; 2001GB-0011037.
PR 29-JUN-2001; 2001US-0895367.
PR 13-JUL-2001; 2001US-0905846.
PR 24-AUG-2001; 2001GB-0020679.
XX
PA (PFIZ) PFIZER LTD.
PA (PFIZ) PFIZER INC.
XX
PI Naylor AM, Van Der Graaf PH, Wayman CP;
XX
DR WPI; 2002-547828/58.
DR N-PSDB; ABN84279, ABN84280.
XX
PT Use of an inhibitor of neuropeptide Y in the preparation of medicament
PT for the treatment or prevention of male erectile dysfunction -
XX
PS Disclosure; Fig 9; 179pp; English.
XX
CC The present sequence is the protein sequence of human SEP, a
CC soluble secreted endopeptidase. The invention relates to the use
CC of an inhibitor of NPY, or an inhibitor of NPY Y1 receptor,
CC especially an inhibitor selective for an NPY or NPY Y1 receptor
CC associated with male genitalia, in the preparation of a medicament
CC for the treatment or prevention of male sexual dysfunction,
CC especially male erectile dysfunction (MED). The NPY inhibitor
CC may be used with an auxiliary active agent such as an SEP
CC inhibitor. The invention provides an assay that can be used to
CC detect candidate inhibitors of SEP. In addition to treatment of
CC MED, NPY inhibitors can also be used to treat abnormal drink and
CC food intake disorders, such as obesity, bulimia, anorexia and
CC metabolic disorders.
XX
SQ Sequence 779 AA;

```
  Query Match           33.7%;  Score 1332.5;  DB 23;  Length 779;
  Best Local Similarity 39.2%;  Pred. No. 2.4e-105;
  Matches  284;  Conservative  145;  Mismatches  258;  Indels   37;  Gaps   17;

Qy      42 QGLLSLQAKQEYCLKPECIEAAAAILSKVNLSVDPCDNFFRFACDGWISNNPIPEDMPSY 101
           :|:   |   | |  | |: ||| ||  :: : :|||:|::||| ||:  : |||    |
Db      77 RGIPEAQEVSEVCTTPGCVIAAARILQNMDPTTEPCDDFYQFACGGWLRRHVIPETNSRY 136

Qy     102 GVYPWLRHNVDLKLKELLEKSISRRRDTEAIQKAKILYSSCMNEKAIEKADAKPLLHILR 161
            ::  ||  ::: || :|| | :  :|  |::||: || ||||:  ||| ::||| ||
Db     137 SIFDVLRDELEVILKAVLENSTA--KDRPAVEKARTLYRSCMNQSVIEKRGSQPLLDIL- 193

Qy     162 HSPFRWPVLESNIGPEGVWSER---KFSLLQTLATFRGQYSNSVFIRLYVSPDDKASNEH 218
               |||           |:|    :: | : ||    |::  | | |::  ||: |: |
Db     194 EVVGGWPVAMDR------WNETVGLEWELERQLALMNSQFNRRVLIDLFIWNDDQNSSRH 247

Qy     219 ILKLDQATLSLAVREDYLDNSTEAKSYRDALYKFMVDTAVLL--GANSSR----AEHDMK 272
           |: :|| || :  || | :  :  |  |:|  :|||  | ||   ||  |     : ||
Db     248 IIYIDQPTLGMPSREYYFNGGSNRK-VREAYLQFMVSVATLLREDANLPRDSCLVQEDMV 306

Qy     273 SVLRLEIKIAEIMIPHENRTSE-AMYNKMNISELSAM--IPQFDWLGYIKKVIDTRLYPH 329
           || || ::|:  :| | |    |:|::| : || :   :  |:|  :|: |: :
Db     307 QVLELETQLAKATVPQEERHDVIALYHRMGLEELQSQFGLKGFNWTLFIQTVLSS----- 361

Qy     330 LK-DISPSENVVVRVPQYFKDLFRILGSERKKTIANYLVWRMVYSRIPNLSRRFQYRWLE 388
           :|  : | | |||    | ::|  |: :   :|| ||||||:|  || :||:||:   :
Db     362 VKIKLLPDEEVVVYGIPYLQNLENIIDTYSARTIQNYLVWRLVLDRIGSLSQRFKDTRVN 421

Qy     389 FSRVIQGTTTLLPQWDKCVNFIESALPYVVGKMFVDVYFQEDKKEMMEELVEGVRWAFID 448
           : : : ||     :| :|| :: | :   || ::|   |  | | |: ||:: ||  |:
Db     422 YRKALFGTMVEEVRWRECVGYVNSNMENAVGSLYVREAFPGDSKSMVRELIDKVRTVFVE 481

Qy     449 MLEKENEWMDAGTKRKAKEKARAVLAKVGYPEFIMNDTH--VNEDLKAIKFSEADYFGNV 506
           |: |  |||  :|:||:||| ::  ::|:|:::|: : :  ::|:   : |||  || |
Db     482 TLD-ELGWMDEESKKKAQEKAMSIREQIGHPDYILEEMNRRLDEEYSNLNFSEDLYFENS 540

Qy     507 LQTRKYLAQSDFFWLRKAVPKTEWFTNPTTVNAFYSASTNQIRFPAGELQKPFFWGTEYP 566
           ||  |  ||     ||: |    |      ||||| : ||| |||| || |||   | |
Db     541 LQNLKVGAQRSLRKLREKVDPNLWIIGAAVVNAFYSPNRNQIVFPAGILQPPFF-SKEQP 599

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Db     600 QALNFGGIGMVIGHEITHGFDDNGRNFDKNGNMMDWWSNFSTQHFREQSECMIYQYGNYS 659

Qy     627 WKKAG-LNVKGKRTLGENIADNGGLREAFRAYRKWINDRRQGLEEPLLPGITFTNNQLFF 685
           |  |   || |  ||||||||||||:|:|::|| ||:    :| ::  |||:  |: ||||
Db     660 WDLADEQNVNGFNTLGENIADNGGVRQAYKAYLKWM---AEGGKDQQLPGLDLTHEQLFF 716

Qy     686 LSYAHVRCNSYRPEAAREQVQIGAHSPPQFRVNGAISNSEEFQKAFNCPPNSTMNRGMDS 745
           ::|| | | ||||| | : ::   ||| ::|| |:: |   |   |:|   : |:   :
Db     717 INYAQVWCGSYRPEFAIQSIKTDVHSPLKYRVLGSLQNLAAFADTFHCARGTPMH-PKER 775

Qy     746 CRLW 749
           ||:|
Db     776 CRVW 779
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RESULT 12
AAU78850
ID AAU78850 standard; Protein; 779 AA.
XX
AC AAU78850;
XX
DT 18-JUN-2002 (first entry)
XX
DE Novel neprilysin family protein, 56638.
XX
KW Neprilysin family; human; gene therapy; protein therapy; vaccine;
KW neprilysin protease; pain; pain associated disorder; tissue injury;
KW chest pain; complex regional pain syndrome; CRPS; headache; migrane;
KW reflex sympathetic dystrophy; RSD; tooth pain; musculoskeletal disorder;
KW joint pain; surgery; inflammation; irritable bowel syndrome; anaemia;
KW aberrant spermatid cell activity; infertility; cancer; brain disorder;

```
KW   cell proliferation disorder; cell differentiation disorder;
KW   cerebral edema; neurodegenerative disease; Alzheimer's disease;
KW   cerebrovascular disease; immune disorder; erythroid associated disorder;
KW   haematopoietic neoplastic disorder; erythroblastosis.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..44
FT                   /label= Signal_peptide
FT   Protein         45..779
FT                   /label= Mature_56628
FT   Domain          572..778
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FT   Region          177..180
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FT   Region          207..210
FT                   /label= N-glycosylation_site
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FT   Region          530..533
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FT   Region          638..641
FT                   /label= N-glycosylation_site
FT   Region          657..660
FT                   /label= N-glycosylation_site
FT   Region          183..186
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FT                   /label= Protein kinase C phosphorylation site
FT   Region          244..246
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FT   Region          269..271
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FT   Region          361..363
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FT                   /label= Protein kinase C phosphorylation site
FT   Region          412..414
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FT   Region          493..495
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FT   Region          735..737
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FT   Region          429..432
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FT                   /label= Casein kinase II phosphorylation site
FT   Region          482..485
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FT                   /label= Casein kinase II phosphorylation site
FT   Region          673..676
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FT   Region          645..653
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FT   Region          750..755
FT                   /label= N-myristoylation_site
FT   Region          776..779
FT                   /label= Prenyl_group_binding_site
XX
PN   WO200226958-A2.
XX
PD   04-APR-2002.
XX
PF   24-SEP-2001; 2001WO-US29905.
XX
PR   25-SEP-2000; 2000US-235035P.
PR   13-AUG-2001; 2001US-0928531.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Bandaru R,  Silos-santiago I;
XX
DR   WPI; 2002-315801/35.
DR   N-PSDB; ABK48251.
XX
PT   Nucleic acids encoding a novel human Neprilysin Protease, useful for
PT   the prevention and treatment of pain -
XX
PS   Claim 5; Fig 1A-D; 123pp; English.
XX
CC   The invention describes nucleic acids (I) encoding a novel human
CC   Neprilysin Protease (II). (I) and (II) may be used in the prevention,
CC   diagnosis and treatment of diseases associated with inappropriate
CC   neprilysin protease expression e.g. by rectifying mutations or deletions
CC   in a patient's genome that affect the activity of the protease by
CC   expressing inactive proteins or to supplement the patients own production
CC   of the protease. (I) And its complementary sequences may also be used as
CC   DNA probes in diagnostic assays to detect and quantitate the presence of
CC   similar nucleic acids in samples, and therefore which patients may be in
CC   need of restorative therapy. (I) and (II) may be useful in the treatment
CC   of pain or pain associated disorders including tissue injury, chest pain,
CC   complex regional pain syndrome (CRPS), reflex sympathetic dystrophy
CC   (RSD), tooth pain; headaches e.g. migrane, and pain associated with
CC   musculoskeletal disorders e.g. joint pain, surgery and inflammation e.g.
CC   irritable bowel syndrome. (II) may also be useful in the treatment of
CC   disorders including anaemia, infertility, aberrant spermatid cell
CC   activity, cell proliferation and/or differentiative disorders e.g. cancer
CC   and brain disorders e.g. cerebral edema, neurodegenerative diseases e.g.
CC   Alzheimer's disease, cerebrovascular disease, haematopoietic neoplastic
CC   disorders, immune disorders and erythroid associated disorders e.g.
CC   erythroblastosis. This is the amino acid sequence of the novel human
CC   neprilysin family protein 566368.
XX
SQ   Sequence   779 AA;

  Query Match             33.7%;  Score 1332.5;  DB 23;  Length 779;
  Best Local Similarity   39.2%;  Pred. No. 2.4e-105;
  Matches  284;  Conservative  145;  Mismatches  258;  Indels   37;  Gaps   17;
```

```
Qy      42 QGLLSLQAKQEYCLKPECIEAAAAILSKVNLSVDPCDNFFRFACDGWISNNPIPEDMPSY 101
           :|:   |   | |  | |: ||| ||  :: : :|||:|::||| ||:  : |||    |
Db      77 RGIPEAQEVSEVCTTPGCVIAAARILQNMDPTTEPCDDFYQFACGGWLRRHVIPETNSRY 136

Qy     102 GVYPWLRHNVDLKLKELLEKSISRRRDTEAIQKAKILYSSCMNEKAIEKADAKPLLHILR 161
            ::  ||  ::: || :|| | :  :|  |::||: || ||||:  |||  ::|||| ||
Db     137 SIFDVLRDELEVILKAVLENSTA--KDRPAVEKARTLYRSCMNQSVIEKRGSQPLLDIL- 193

Qy     162 HSPFRWPVLESNIGPEGVWSER---KFSLLQTLATFRGQYSNSVFIRLYVSPDDKASNEH 218
               |||          |:|    :: | : ||    |::  | | |::  ||: |: |
Db     194 EVVGGWPVAMDR------WNETVGLEWELERQLALMNSQFNRRVLIDLFIWNDDQNSSRH 247

Qy     219 ILKLDQATLSLAVREDYLDNSTEAKSYRDALYKFMVDTAVLL--GANSSR----AEHDMK 272
           |: :|| || :  || | :  :  |  |:|  :|||  | ||   ||  |     : ||
Db     248 IIYIDQPTLGMPSREYYFNGGSNRK-VREAYLQFMVSVATLLREDANLPRDSCLVQEDMV 306

Qy     273 SVLRLEIKIAEIMIPHENRTSE-AMYNKMNISELSAM--IPQFDWLGYIKKVIDTRLYPH 329
            || || ::|:  :| | |    |:|::| : || :   :  |:|  :|: |: :
Db     307 QVLELETQLAKATVPQEERHDVIALYHRMGLEELQSQFGLKGFNWTLFIQTVLSS----- 361

Qy     330 LK-DISPSENVVVRVPQYFKDLFRILGSERKKTIANYLVWRMVYSRIPNLSRRFQYRWLE 388
           :|  : | | |||    | ::|  |: :   :|| |||||:|  || :||:||:   :
Db     362 VKIKLLPDEEVVVYGIPYLQNLENIIDTYSARTIQNYLVWRLVLDRIGSLSQRFKDTRVN 421

Qy     389 FSRVIQGTTTLLPQWDKCVNFIESALPYVVGKMFVDVYFQEDKKEMMEELVEGVRWAFID 448
           : : : ||     :| :|| :: | :   || ::|   |  | | |: ||:: ||  |::
Db     422 YRKALFGTMVEEVRWRECVGYVNSNMENAVGSLYVREAFPGDSKSMVRELIDKVRTVFVE 481

Qy     449 MLEKENEWMDAGTKRKAKEKARAVLAKVGYPEFIMNDTH--VNEDLKAIKFSEADYFGNV 506
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Db     482 TLD-ELGWMDEESKKKAQEKAMSIREQIGHPDYILEEMNRRLDEEYSNLNFSEDLYFENS 540

Qy     507 LQTRKYLAQSDFFWLRKAVPKTEWFTNPTTVNAFYSASTNQIRFPAGELQKPFFWGTEYP 566
           ||  |  ||     ||: |    |      |||||| : ||| |||| || |||   | |
Db     541 LQNLKVGAQRSLRKLREKVDPNLWIIGAAVVNAFYSPNRNQIVFPAGILQPPFF-SKEQP 599

Qy     567 RSLSYGAIGVIVGHEFTHGFDNNGRKYDKNGNLDPWWSTESEEKFKEKTKCMINQYSNYY 626
           ::|::| ||:::||| |||||:||| :|||||:  |||  | : |:|:::||| || ||
Db     600 QALNFGGIGMVIGHEITHGFDDNGRNFDKNGNMMDWWSNFSTQHFREQSECMIYQYGNYS 659

Qy     627 WKKAG-LNVKGKRTLGENIADNGGLREAFRAYRKWINDRRQGLEEPLLPGITFTNNQLFF 685
           |  |   || |  |||||||||||:|:|::|| ||:    :| ::  |||:  |: |||| 
Db     660 WDLADEQNVNGFNTLGENIADNGGVRQAYKAYLKWM---AEGGKDQQLPGLDLTHEQLFF 716

Qy     686 LSYAHVRCNSYRPEAAREQVQIGAHSPPQFRVVNGAISNSEEFQKAFNCPPNSTMNRGMDS 745
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Db     717 INYAQVWCGSYRPEFAIQSIKTDVHSPLKYRVLGSLQNLAAFADTFHCARGTPMH-PKER 775

Qy     746 CRLW 749
           ||:|
Db     776 CRVW 779


RESULT 13
AAE17779
ID   AAE17779 standard; Protein; 779 AA.
XX
AC   AAE17779;
XX
DT   07-MAY-2002  (first entry)
XX
DE   Human soluble secreted endopeptidase (SEP) protein.
XX
KW   Human; secreted endopeptidase; SEP; endocrine; vasotropic; analgesic;
KW   enzyme; gynaecological; antisense-therapy; male erectile dysfunction;
KW   MED; female sexual dysfunction; FSD; female sexual arousal disorder;
KW   FSAD; premature ejaculation; anorgasmia; vaginismus.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Domain          570..779
FT                   /label= Catalytic_domain
XX
OS   Homo sapiens.
XX
PN   WO200206492-A1.
XX
PD   24-JAN-2002.
XX
PF   16-JUL-2001; 2001WO-IB01263.
XX
PR   14-JUL-2000; 2000GB-0017387.
XX
PA   (PFIZ ) PFIZER LTD.
PA   (PFIZ ) PFIZER INC.
XX
PI   Harrow ID,  Stacey P,  Walsh RT,  Wayman CP,  Wayman CP,  Phillips SC;
XX
DR   WPI; 2002-155042/20.
DR   N-PSDB; AAD28544.
XX
PT   An isolated and/or purified nucleic acid encoding a human soluble
PT   secreted endopeptidase which is useful for treating sexual dysfunction,
PT   for e.g. male erectile dysfunction or female sexual dysfunction such as
PT   female sexual arousal disorder -
XX
PS   Claim 4; Page 162; 167pp; English.
XX
CC   The invention relates to an isolated and/or purified nucleic acid
CC   encoding a human soluble secreted endopeptidase (SEP). The anti-SEP
CC   antibody and the compound which inhibits or selectively inhibits the
CC   human SEP protein are useful in the manufacture of a medicament for
CC   the prophylaxis and/or treatment of sexual dysfunction, in particular
CC   male erectile dysfunction (MED) or female sexual dysfunction (FSD)
CC   (e.g. female sexual arousal disorder (FSAD)). The SEP polypeptides are
CC   also useful for treating the above disorders and other disorders such
CC   as premature ejaculation, anorgasmia, sexual pain (e.g. vaginismus) and
CC   hypoactive sexual desire disorder. The present sequence is human SEP
CC   protein.
XX
SQ   Sequence   779 AA;

  Query Match           33.7%;  Score 1332.5;  DB 23;  Length 779;
  Best Local Similarity   39.2%;  Pred. No. 2.4e-105;
  Matches  284;  Conservative  145;  Mismatches  258;  Indels   37;  Gaps   17;

Qy      42 QGLLSLQAKQEYCLKPECIEAAAAILSKVNLSVDPCDNFFRFACDGWISNNPIPEDMPSY 101
           :|:   |   | |  | |: ||| ||  :: : :|||:|::||| ||:  : |||    |
Db      77 RGIPEAQEVSEVCTTPGCVIAAARILQNMDPTTEPCDDFYQFACGGWLRRHVIPETNSRY 136

Qy     102 GVYPWLRHNVDLKLKELLEKSISRRRDTEAIQKAKILYSSCMNEKAIEKADAKPLLHILR 161
            ::  ||  ::: || :|| | :  :|  |::||: || ||||:  |||  ::|||| ||
Db     137 SIFDVLRDELEVILKAVLENSTA--KDRPAVEKARTLYRSCMNQSVIEKRGSQPLLDIL- 193

Qy     162 HSPFRWPVLESNIGPEGVWSER---KFSLLQTLATFRGQYSNSVFIRLYVSPDDKASNEH 218
               |||          |:|    :: | : ||    |::  | | |::  ||: |: |
Db     194 EVVGGWPVAMDR------WNETVGLEWELERQLALMNSQFNRRVLIDLFIWNDDQNSSRH 247

Qy     219 ILKLDQATLSLAVREDYLDNSTEAKSYRDALYKFMVDTAVLL--GANSSR----AEHDMK 272
           |: :|| || :  || | :  :  |  |:|  :|||  | ||   ||  |     : ||
Db     248 IIYIDQPTLGMPSREYYFNGGSNRK-VREAYLQFMVSVATLLREDANLPRDSCLVQEDMV 306

Qy     273 SVLRLEIKIAEIMIPHENRTSE-AMYNKMNISELSAM--IPQFDWLGYIKKVIDTRLYPH 329
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Db     307 QVLELETQLAKATVPQEERHDVIALYHRMGLEELQSQFGLKGFNWTLFIQTVLSS----- 361

Qy     330 LK-DISPSENVVVRVPQYFKDLFRILGSERKKTIANYLVWRMVYSRIPNLSRRFQYRWLE 388
           :|  : | | |||    | ::|  |: :   :|| |||||:|  || :||:||:   :
Db     362 VKIKLLPDEEVVVYGIPYLQNLENIIDTYSARTIQNYLVWRLVLDRIGSLSQRFKDTRVN 421

Qy     389 FSRVIQGTTTLLPQWDKCVNFIESALPYVVGKMFVDVYFQEDKKEMMEELVEGVRWAFID 448
           : : : ||     :| :|| :: | :   || ::|   |  | | |: ||:: ||  |::
Db     422 YRKALFGTMVEEVRWRECVGYVNSNMENAVGSLYVREAFPGDSKSMVRELIDKVRTVFVE 481
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Qy     449 MLEKENEWMDAGTKRKAKEKARAVLAKVGYPEFIMNDTH--VNEDLKAIKFSEADYFGNV 506
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Qy     507 LQTRKYLAQSDFFWLRKAVPKTEWFTNPTTVNAFYSASTNQIRFPAGELQKPFFWGTEYP 566
Db     541 LQNLKVGAQRSLRKLREKVDPNLWIIGAAVVNAFYSPNRNQIVFPAGILQPPFF-SKEQP 599

Qy     567 RSLSYGAIGVIVGHEFTHGFDNNGRKYDKNGNLDPWWSTESEEKFKEKTKCMINQYSNYY 626
Db     600 QALNFGGIGMVIGHEITHGFDDNGRNFDKNGNMMDWWSNFSTQHFREQSECMIYQYGNYS 659

Qy     627 WKKAG-LNVKGKRTLGENIADNGGLREAFRAYRKWINDRRQGLEEPLLPGITFTNNQLFF 685
Db     660 WDLADEQNVNGFNTLGENIADNGGVRQAYKAYLKWM---AEGGKDQQLPGLDLTHEQLFF 716

Qy     686 LSYAHVRCNSYRPEAAREQVQIGAHSPPQFRVNGAISNSEEFQKAFNCPPNSTMNRGMDS 745
Db     717 INYAQVWCGSYRPEFAIQSIKTDVHSPLKYRVLGSLQNLAAFADTFHCARGTPMH-PKER 775

Qy     746 CRLW 749
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RESULT 14
AAB83844
ID   AAB83844 standard; Protein; 702 AA.
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AC   AAB83844;
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DT   23-JUL-2001  (first entry)
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DE   Amino acid sequence of a His-tagged metalloprotease enzyme IGS5.
XX
KW   Metalloprotease; IGS5; infection; pain; cancer; diabetes; obesity;
KW   anorexia; bulimia; asthma; Parkinson's disease; acute heart failure;
KW   hypotension; hypertension; urinary retention; osteoporosis;
KW   angina pectoris; myocardial infarction; stroke; ulcer; allergy;
KW   benign prostatic hypertrophy; migraine; psychotic disorder;
KW   neurological disorder; autism; multiple sclerosis; Alzheimer's disease;
KW   neurodegenerative disease; sleep disorder; epilepsy; kidney disease;
KW   cardiovascular disease; arteriosclerosis; cerebrovasospasm;
KW   subarachnoid hemorrhage; cerebral ischemia; cerebral infarction;
KW   peripheral vascular disease; Raynaud's disease; motility disorder;
KW   gastrointestinal disorder; gastric emptying; gastroparesis; diarrhoea;
KW   inflammation; chemotherapy induced injury; tumour invasion;
KW   immune disorder; arthritis; endotoxin shock; sepsis; diabetes mellitus;
KW   severe mental retardation; dyskinesia; Huntington's disease;
KW   Gilles de la Tourette's syndrome.
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OS   Homo sapiens.
XX
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FT                   /note= "N-glycosylation site"
FT   Modified-site   130
FT                   /note= "N-glycosylation site"
FT   Modified-site   166
FT                   /note= "N-glycosylation site"
FT   Modified-site   273
FT                   /note= "N-glycosylation site"
FT   Modified-site   453
FT                   /note= "N-glycosylation site"
FT   Modified-site   561
FT                   /note= "N-glycosylation site"
FT   Modified-site   580
FT                   /note= "N-glycosylation site"
XX
PN   WO200136610-A1.
XX
PD   25-MAY-2001.
XX
PF   17-NOV-2000; 2000WO-EP11532.
XX
PR   19-NOV-1999;   99EP-0203862.
PR   19-NOV-1999;   99NL-1013616.
PR   31-MAY-2000; 2000EP-0201937.
PR   31-MAY-2000; 2000NL-1015356.
XX
PA   (SOLV ) SOLVAY PHARM BV.
XX
PI   Deleersnijder W,  Wiegers R,  Weske M;
XX
DR   WPI; 2001-343815/36.
XX
PT   New IGS5 polypeptides useful for treating infections, pain, cancer,
PT   diabetes, obesity, anorexia, bulimia, asthma, schizophrenia,
PT   hypertension, urinary retention and Parkinson's disease -
XX
PS   Example 6c; Fig 6; 115pp; English.
XX
CC   The present sequence represents a His-tagged metalloprotease designated
CC   IGS5. IGS5 polynucleotides and polypeptides are useful for treating
CC   infections, pain, cancer, diabetes, obesity, anorexia, bulimia, asthma,
CC   Parkinson's disease, acute heart failure, hypotension, hypertension,
CC   urinary retention, osteoporosis, angina pectoris, myocardial infarction,
CC   stroke, ulcers, allergies, benign prostatic hypertrophy, migraine,
CC   psychotic and neurological disorders, autism, multiple sclerosis,
CC   Alzheimer's disease, and other neurodegenerative diseases, sleep
CC   disorder, epilepsy, cardiovascular diseases, arteriosclerosis,
CC   cerebrovasospasm, subarachnoid hemorrhage, cerebral ischemia, cerebral
CC   infarction, peripheral vascular disease, Raynaud's disease, kidney
CC   diseases, gastrointestinal disorders, motility disorders and conditions
CC   of delayed gastric emptying, post-operative or diabetic gastroparesis,
CC   diarrhoea, inflammations, chemotherapy induced injury, tumour invasion,
CC   immune disorders, arthritis, endotoxin shock, sepsis, complications of
CC   diabetes mellitus, and severe mental retardation and dyskinesias, such
CC   as Huntington's disease or Gilles de la Tourette's syndrome.
XX
SQ   Sequence   702 AA;
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Query Match 33.5%; Score 1326.5; DB 22; Length 702;
Best Local Similarity 39.5%; Pred. No. 6.7e-105;
Matches 282; Conservative 143; Mismatches 252; Indels 37; Gaps 17;

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Qy      52 EYCLKPECIEAAAAILSKVNLSVDPCDNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNV 111
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Qy     112 DLKLKELLEKSISRRRDTEAIQKAKILYSSCMNEKAIEKADAKPLLHILRHSPFRWPVLE 171
Db      70 EVILKAVLENSTA--KDRPAVEKARTLYRSCMNQSVIEKRGSQPLLDIL-EVVGGWPVAM 126

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Qy     229 LAVREDYLDNSTEAKSYRDALYKFMVDTAVLL--GANSSR----AEHDMKSVLRLEIKIA 282
Db     181 MPSREYYFNGGSNRK-VREAYLQFMVSVATLLREDANLPRDSCLVQEDMMQVLELETQLA 239

Qy     283 EIMIPHENRTSE-AMYNKMNISELSAM--IPQFDWLGYIKKVIDTRLYPHLK-DISPSEN 338
Db     240 KATVPQEERHDVIALYHRMGLEELQSQFGLKGFNWTLFIQTVLSS-----VKIKLLPDEE 294

Qy     339 VVVRVPQYFKDLFRILGSERKKTIANYLVWRMVYSRIPNLSRRFQYRWLEFSRVIQGTTT 398
Db     295 VVVYGIPYLQNLENIIDTYSARTIQNYLVWRLVLDRIGSLSQRFKDTRVNYRKALFGTMV 354

Qy     399 LLPQWDKCVNFIESALPYVVGKMFVDVYFQEDKKEMMEELVEGVRWAFIDMLEKENEWMD 458
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Qy     459 AGTKRKAKEKARAVLAKVGYPEFIMNDTH--VNEDLKAIKFSEADYFGNVLQTRKYLAQS 516
           :|:||:||| ::  ::|:|::|: : :  ::|:   : ||| || | ||  |  ||
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Db     533 VIGHEITHGFDDNGRNFDKNGNMMDWWSNFSTQHFREQSECMIYQYGNYSWDLADEQNVN 592

Qy     636 GKRTLGENIADNGGLREAFRAYRKWINDRRQGLEEPLLPGITFTNNQLFFLSYAHVRCNS 695
           |  |||||||||||:|:|::|| ||:    :| ::  |||:  |: ||||::|| | | |
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RESULT 15
AAB83840
ID   AAB83840 standard; Protein; 691 AA.
XX
AC   AAB83840;
XX
DT   23-JUL-2001  (first entry)
XX
DE   Amino acid sequence of a human metalloprotease enzyme IGS5.
XX
KW   Metalloprotease; IGS5; infection; pain; cancer; diabetes; obesity;
KW   anorexia; bulimia; asthma; Parkinson's disease; acute heart failure;
KW   hypotension; hypertension; urinary retention; osteoporosis;
KW   angina pectoris; myocardial infarction; stroke; ulcer; allergy;
KW   benign prostatic hypertrophy; migraine; psychotic disorder;
KW   neurological disorder; autism; multiple sclerosis; Alzheimer's disease;
KW   neurodegenerative disease; sleep disorder; epilepsy; kidney disease;
KW   cardiovascular disease; arteriosclerosis; cerebrovasospasm;
KW   subarachnoid hemorrhage; cerebral ischemia; cerebral infarction;
KW   peripheral vascular disease; Raynaud's disease; motility disorder;
KW   gastrointestinal disorder; gastric emptying; gastroparesis; diarrhoea;
KW   inflammation; chemotherapy induced injury; tumour invasion;
KW   immune disorder; arthritis; endotoxin shock; sepsis; diabetes mellitus;
KW   severe mental retardation; dyskinesia; Huntington's disease;
KW   Gilles de la Tourette's syndrome.
XX
OS   Homo sapiens.
XX
PN   WO200136610-A1.
XX
PD   25-MAY-2001.
XX
PF   17-NOV-2000; 2000WO-EP11532.
XX
PR   19-NOV-1999;   99EP-0203862.
PR   19-NOV-1999;   99NL-1013616.
PR   31-MAY-2000; 2000EP-0201937.
PR   31-MAY-2000; 2000NL-1015356.
XX
PA   (SOLV ) SOLVAY PHARM BV.
XX
PI   Deleersnijder W,  Wiegers R,  Weske M;
XX
DR   WPI; 2001-343815/36.
DR   N-PSDB; AAF89737.
XX
PT   New IGS5 polypeptides useful for treating infections, pain, cancer,
PT   diabetes, obesity, anorexia, bulimia, asthma, schizophrenia,
PT   hypertension, urinary retention and Parkinson's disease  -
XX
PS   Claim 3; Page 6; 115pp; English.
XX
CC   The present sequence represents a human metalloprotease enzyme designated
CC   IGS5. IGS5 polynucleotides and polypeptides are useful for treating
CC   infections, pain, cancer, diabetes, obesity, anorexia, bulimia, asthma,
CC   Parkinson's disease, acute heart failure, hypotension, hypertension,
CC   urinary retention, osteoporosis, angina pectoris, myocardial infarction,
CC   stroke, ulcers, allergies, benign prostatic hypertrophy, migraine,
CC   psychotic and neurological disorders, autism, multiple sclerosis,
CC   Alzheimer's disease, and other neurodegenerative diseases, sleep
CC   disorder, epilepsy, cardiovascular diseases, arteriosclerosis,
CC   cerebrovasospasm, subarachnoid hemorrhage, cerebral ischemia, cerebral
CC   infarction, peripheral vascular disease, Raynaud's disease, kidney
CC   diseases, gastrointestinal disorders, motility disorders and conditions
CC   of delayed gastric emptying, post-operative or diabetic gastroparesis,
CC   diarrhoea, inflammations, chemotherapy induced injury, tumour invasion,
CC   immune disorders, arthritis, endotoxin shock, sepsis, complications of
CC   diabetes mellitus, and severe mental retardation and dyskinesias, such
CC   as Huntington's disease or Gilles de la Tourette's syndrome.
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Qy     461 TKRKAKEKARAVLAKVGYPEFIMNDTH--VNEDLKAIKFSEADYFGNVLQTRKYLAQSDF 518
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Db     524 GHEITHGFDDNGRNFDKNGNMMDWWSNFSTQHFREQSECMIYQYGNYSWDLADEQNVNGF 583

Qy     638 RTLGENIADNGGLREAFRAYRKWINDRRQGLEEPLLPGITFTNNQLFFLSYAHVRCNSYR 697
           |||||||||||:|:|::|| ||:    :| ::  |||:  |: ||||::|| | | |||
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Job time : 84 secs

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OM protein - protein search, using sw model

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Title: US-09-913-955A-1
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1257	31.8	703	3	US-08-646-273-25	Sequence 25, Appl
2	1257	31.8	753	3	US-08-646-273-36	Sequence 36, Appl
3	1248.5	31.5	758	1	US-08-289-112-2	Sequence 2, Appli
4	1241.5	31.4	708	3	US-08-646-273-23	Sequence 23, Appl
5	1241.5	31.4	754	3	US-08-646-273-30	Sequence 30, Appl
6	1184	29.9	787	1	US-08-574-763-2	Sequence 2, Appli
7	983.5	24.8	775	4	US-09-305-640-2	Sequence 2, Appli
8	963.5	24.3	567	3	US-08-646-273-19	Sequence 19, Appl
9	527.5	13.3	189	3	US-08-646-273-14	Sequence 14, Appl
10	246	6.2	181	4	US-09-305-640-4	Sequence 4, Appli
11	116	2.9	725	2	US-08-813-940-25	Sequence 25, Appl
12	114.5	2.9	990	2	US-08-392-625-20	Sequence 20, Appl
13	114.5	2.9	990	2	US-08-466-961A-20	Sequence 20, Appl
14	114.5	2.9	990	2	US-08-645-193B-15	Sequence 15, Appl
15	108	2.7	681	2	US-08-655-345-4	Sequence 4, Appli
16	108	2.7	681	3	US-09-183-275-4	Sequence 4, Appli
17	108	2.7	681	5	PCT-US96-08407-4	Sequence 4, Appli
18	108	2.7	698	4	US-09-727-169-4	Sequence 4, Appli
19	108	2.7	698	4	US-09-579-766A-4	Sequence 4, Appli
20	108	2.7	807	2	US-08-655-345-2	Sequence 2, Appli
21	108	2.7	807	3	US-09-183-275-2	Sequence 2, Appli
22	108	2.7	807	5	PCT-US96-08407-2	Sequence 2, Appli
23	108	2.7	824	4	US-09-727-169-2	Sequence 2, Appli
24	108	2.7	824	4	US-09-579-766A-2	Sequence 2, Appli
25	106.5	2.7	803	1	US-08-062-368-2	Sequence 2, Appli
26	105.5	2.7	548	4	US-09-601-091-2	Sequence 2, Appli
27	105	2.7	479	1	US-08-484-105-10	Sequence 10, Appl
28	105	2.7	479	1	US-08-484-106-10	Sequence 10, Appl
29	103.5	2.6	548	4	US-09-601-091-4	Sequence 4, Appli
30	103.5	2.6	548	4	US-09-398-395A-52	Sequence 52, Appl
31	103.5	2.6	878	4	US-09-255-829-12	Sequence 12, Appl
32	103.5	2.6	907	4	US-09-255-829-16	Sequence 16, Appl
33	103.5	2.6	953	4	US-09-255-829-14	Sequence 14, Appl
34	103.5	2.6	1013	4	US-09-255-829-18	Sequence 18, Appl
35	103	2.6	871	4	US-09-255-829-2	Sequence 2, Appli
36	103	2.6	871	4	US-09-255-829-8	Sequence 8, Appli
37	103	2.6	871	4	US-09-255-829-26	Sequence 26, Appl
38	103	2.6	873	4	US-09-255-829-6	Sequence 6, Appli
39	103	2.6	894	4	US-09-255-829-4	Sequence 4, Appli
40	103	2.6	1296	1	US-08-480-604A-28	Sequence 28, Appl
41	103	2.6	1296	2	US-08-405-496A-28	Sequence 28, Appl
42	103	2.6	1296	4	US-08-915-136-28	Sequence 28, Appl
43	103	2.6	2291	2	US-08-286-819A-29	Sequence 29, Appl
44	103	2.6	2291	3	US-08-980-357-29	Sequence 29, Appl
45	101.5	2.6	607	4	US-09-134-001C-2994	Sequence 2994, Ap

ALIGNMENTS

RESULT 1
US-08-646-273-25
; Sequence 25, Application US/08646273
; Patent No. 6066502
; GENERAL INFORMATION:
; APPLICANT: Kroeger, Burkhard, Seulberger, Harald, Meyer, Thomas, Schmidt,
; APPLICANT: Martin, Jacob, Elard, Otter, Rainer, Subkowski, Thomas, Hillen, Hein
; TITLE OF INVENTION: Endothelin Converting Enzyme (ECE).
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Keil & Weinkauf
; STREET: 1101 Connecticut Avenue
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
; COMPUTER: IBM AT-compatible, 80486 processor
; OPERATING SYSTEM: MS-DOS version 6.0
; SOFTWARE: WordPerfect version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,273
; FILING DATE: 16-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP94/03706
; FILING DATE: 11-NOV-1994
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 703 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-646-273-25

Query Match 31.8%; Score 1257; DB 3; Length 703;
Best Local Similarity 37.6%; Pred. No. 5.6e-115;
Matches 281; Conservative 126; Mismatches 276; Indels 64; Gaps 21;

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Qy      21 IALVVFVGGTLVLGTILFLVSQGLLSLQAKQEYCLKPECIEAAAAILSKVNLSVDPCDNF 80
           : |||      |  | :  | : |:          ||   |:   ::||| :: :|||| :|
Db       3 VVLVVL----LAAGLVACLAALGIQYQTRSPSVCLSEACVSVTSSILSSMDPTVDPCHDF 58

Qy      81 FRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLEKSISRRRDTEAIQKAKILYS 140
           | :|| |||  ||:|:    :| :  |  :    :| ||| | :    :|| :||:: |
Db      59 FSYACGGWIKANPVPDGHSRWGTFSNLWEHNQAIIKHLLENSTA--SVSEAERKAQVYYR 116

Qy     141 SCMNEKAIEKADAKPLLHILRHSPFRWPVLESNIGPEGVWSERKFSLLQTLATFRGQYSN 200
```

```
           :||||  ||:  ||||: ::      | :       | |::  |    ||      |
Db    117 ACMNETRIEELRAKPLMELIERLG-GWNI-------TGPWAKDNFQ--DTLQVVTAHYRT 166

Qy    201 SVFIRLYVSPDDKASNEHILKLDQATLSLAVREDYLDNSTEAKSYRDALYKFMVDTAVLL 260
          | |  :||| | | || ::::::||: | |  |: || | || :        :||    ||
Db    167 SPFFSVYVSADSKNSNSNVIQVDQSGLGLPSRDYYL-NKTENEKVLTGYLNYMVQLGKLL 225

Qy    261 GANSSRA-EHDMKSVLRLEIKIAEIMIPHENRTSEAM-YNKMNISELSAMIPQFDWLGYI 318
          |     |    |: :|  |  :| | || | |  | : |:|:  :||  : |  :|| :
Db    226 GGGDEEAIRPQMQQILDFETALANITIPQEKRRDEELIYHKVTAAELQTLAPAINWLPF- 284

Qy    319 KKVIDTRLYPHLKDISPSENVVVRVPQYFKDLFRILGSERKKTIANYLVWRMVYSRIPNL 378
          ::|  ||   :|: || :||   :| : :  :: :  :  : ||::| :|       |
Db    285 ---LNTIFYP--VEINESEPIVVYDKEYLEQISTLINTTDRCLLNNYMIWNLVRKTSSFL 339

Qy    379 SRRFQYRWLEFSRVIQGT-TTLLPQWDKCVNFIESALPYVVGKMFVDVYFQEDKKEMMEE 437
          :|||    :|  |: ||  | ||:|  ||:  |: | : :| |||   | || | :  |
Db    340 DQRFQDADEKFMEVMYGTKKTCLPRWKFCVSDTENNLGFALGPMFVKATFAEDSKSIATE 399

Qy    438 LVEGVRWAFIDMLEKENEWMDAGTKRKAKEKARAVLAKVGYPEFIM---------NDTHV 488
          ::  :: || : |    :|||  |:: ||||| |:   :||| |||          ||
Db    400 IILEIKKAFEESL-STLKWMDEETRKSAKEKADAIYNMIGYPNFIMDPKELDKVFNDYTA 458

Qy    489 NEDLKAIKFSEADYFGNVLQTRKYLAQSDFFW------LRKAVPKTEWFTNPTTVNAFYS 542
          ||          || | ::       :| |      ||||  : :|   |  |||:||
Db    459 VPDL---------YFENAMRF------FNFSWRVTADQLRKAPNRDQWSMTPPMVNAYYS 503

Qy    543 ASTNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNGRKYDKNGNLDPW 602
          : |:| |||| || ||:  :  |::|::| |||:|||| || ||: ||:|||:||| ||
Db    504 PTKNEIVFPAGILQAPFYTRSS-PKALNFGGIGVVVGHELTHAFDDQGREYDKDGNLRPW 562

Qy    603 WSTESEEKFKEKTKCMINQYSNYYWKKAGLNVKGKRTLGENIADNGGLREAFRAYRKWIN 662
          |   | | || :|:||: |||||      |  | |: |||||||||||: |:|||: |:
Db    563 WKNSSVEAFKRQTECMVEQYSNY--SVNGEPVNGRHTLGENIADNGGLKAAYRAYQNWV- 619

Qy    663 DRRQGLEEPLLPGITFTNNQLFFLSYAHVRCNSYRPEAAREQVQIGAHSPPQFRVNGAIS 722
          :: | |   || :  |||||||| :| | |:   ||:: | :    ||| :||| |::|
Db    620 -KKNGAEHS-LPTLGLTNNQLFFLGFAQVWCSVRTPESSHEGLITDPHSPSRFRVIGSLS 677

Qy    723 NSEEFQKAFNCPPNSTMNRGMDSCRLW 749
          ||:|| : | ||| | ||     | :|
Db    678 NSKEFSEHFRCPPGSPMN-PPHKCEVW 703


RESULT 2
US-08-646-273-36
; Sequence 36, Application US/08646273
; Patent No. 6066502
;  GENERAL INFORMATION:
;    APPLICANT:  Kroeger, Burkhard, Seulberger, Harald, Meyer, Thomas, Schmidt,
;    APPLICANT:  Martin, Jacob, Elard, Otter, Rainer, Subkowski, Thomas, Hillen, Heinz.
;    TITLE OF INVENTION:  Endothelin Converting Enzyme (ECE).
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Keil & Weinkauf
;      STREET:  1101 Connecticut Avenue
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 1.4 Mb storage
;      COMPUTER:  IBM AT-compatible, 80486 processor
;      OPERATING SYSTEM:  MS-DOS version 6.0
;      SOFTWARE:  WordPerfect version 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/646,273
;      FILING DATE:  16-NOV-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/EP94/03706
;      FILING DATE:  11-NOV-1994
;  INFORMATION FOR SEQ ID NO:  36:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  753 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-646-273-36

  Query Match             31.8%;  Score 1257;  DB 3;  Length 753;
  Best Local Similarity   37.6%;  Pred. No. 6.3e-115;
  Matches  281;  Conservative  126;  Mismatches  276;  Indels   64;  Gaps   21;

Qy      21 IALVVFVGGTLVLGTILFLVSQGLLSLQAKQEYCLKPECIEAAAAILSKVNLSVDPCDNF 80
           : |||     |  | :  | : |:          ||   |:   ::||| :: :|||| :|
Db      53 VVLVVL----LAAGLVACLAALGIQYQTRSPSVCLSEACVSVTSSILSSMDPTVDPCHDF 108

Qy      81 FRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLEKSISRRRDTEAIQKAKILYS 140
           | :|| |||  ||:|:    :| : |  :    :| ||| | :    :|| :||:: |
Db     109 FSYACGGWIKANPVPDGHSRWGTFSNLWEHNQAIIKHLLENSTA--SVSEAERKAQVYYR 166

Qy     141 SCMNEKAIEKADAKPLLHILRHSPFRWPVLESNIGPEGVWSERKFSLLQTLATFRGQYSN 200
           :|||  ||:  ||||: ::       | :       | |::  |    ||      |
Db     167 ACMNETRIEELRAKPLMELIERLG-GWNI-------TGPWAKDNFQ--DTLQVVTAHYRT 216

Qy     201 SVFIRLYVSPDDKASNEHILKLDQATLSLAVREDYLDNSTEAKSYRDALYKFMVDTAVLL 260
           | |  :||| | | || :::::||: | |  |: || | || :        :||    ||
Db     217 SPFFSVYVSADSKNSNSNVIQVDQSGLGLPSRDYYL-NKTENEKVLTGYLNYMVQLGKLL 275

Qy     261 GANSSRA-EHDMKSVLRLEIKIAEIMIPHENRTSEAM-YNKMNISELSAMIPQFDWLGYI 318
           |     |    |: :|  |  :| | || | |  | : |:|:  :||  : |  :|| :
Db     276 GGGDEEAIRPQMQQILDFETALANITIPQEKRRDEELIYHKVTAAELQTLAPAINWLPF- 334

Qy     319 KKVIDTRLYPHLKDISPSENVVVRVPQYFKDLFRILGSERKKTIANYLVWRMVYSRIPNL 378
           ::|  ||   :|: || :||   :| : :  :: :  :  : ||::| :|       |
Db     335 ---LNTIFYP--VEINESEPIVVYDKEYLEQISTLINTTDRCLLNNYMIWNLVRKTSSFL 389

Qy     379 SRRFQYRWLEFSRVIQGT-TTLLPQWDKCVNFIESALPYVVGKMFVDVYFQEDKKEMMEE 437
           :|||    :|  |: ||  | ||:|  ||:  |: | : :| |||   | || | :  |
Db     390 DQRFQDADEKFMEVMYGTKKTCLPRWKFCVSDTENNLGFALGPMFVKATFAEDSKSIATE 449

Qy     438 LVEGVRWAFIDMLEKENEWMDAGTKRKAKEKARAVLAKVGYPEFIM---------NDTHV 488
           ::  :: || : |    :|||  |:: ||||| |:   :||| |||          ||
Db     450 IILEIKKAFEESL-STLKWMDEETRKSAKEKADAIYNMIGYPNFIMDPKELDKVFNDYTA 508

Qy     489 NEDLKAIKFSEADYFGNVLQTRKYLAQSDFFW------LRKAVPKTEWFTNPTTVNAFYS 542
           ||          || | ::       :| |      ||||  : :|   |  |||:||
Db     509 VPDL---------YFENAMRF------FNFSWRVTADQLRKAPNRDQWSMTPPMVNAYYS 553

Qy     543 ASTNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNGRKYDKNGNLDPW 602
           : |:| |||| || ||:  :  |::|::| |||:|||| || ||: ||:|||:||| ||
Db     554 PTKNEIVFPAGILQAPFYTRSS-PKALNFGGIGVVVGHELTHAFDDQGREYDKDGNLRPW 612

Qy     603 WSTESEEKFKEKTKCMINQYSNYYWKKAGLNVKGKRTLGENIADNGGLREAFRAYRKWIN 662
           |   | | || :|:||: |||||      |  | |: |||||||||||: |:|||: |:
Db     613 WKNSSVEAFKRQTECMVEQYSNY--SVNGEPVNGRHTLGENIADNGGLKAAYRAYQNWV- 669

Qy     663 DRRQGLEEPLLPGITFTNNQLFFLSYAHVRCNSYRPEAAREQVQIGAHSPPQFRVNGAIS 722
           :: | |   || :  |||||||| :| | |:   ||:: | :    ||| :||| |::|
Db     670 -KKNGAEHS-LPTLGLTNNQLFFLGFAQVWCSVRTPESSHEGLITDPHSPSRFRVIGSLS 727

Qy     723 NSEEFQKAFNCPPNSTMNRGMDSCRLW 749
           ||:|| : | ||| | ||     | :|
Db     728 NSKEFSEHFRCPPGSPMN-PPHKCEVW 753


RESULT 3
US-08-289-112-2
; Sequence 2, Application US/08289112
; Patent No. 5688640
;  GENERAL INFORMATION:
;    APPLICANT:  Yanagisawa, Masashi
;    TITLE OF INVENTION:  Endothelin Converting Enzyme-1: A
;    TITLE OF INVENTION:  Membrane-Bound Metalloprotease That Catalyzes The
;    TITLE OF INVENTION:  Proteolytic Activation of Big Endothelin-1
```

```
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Arnold, White & Durkee
;      STREET:  P.O. Box 4433
;      CITY:  Houston
;      STATE:  TX
;      COUNTRY:  USA
;      ZIP:  77210-4433
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/289,112
;      FILING DATE:  10-APR-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Parker, David L.
;      REGISTRATION NUMBER:  32,165
;      REFERENCE/DOCKET NUMBER:  UTSD:414/PAR
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713-787-1400
;      TELEFAX:  713-789-2679
;      TELEX:  79-0924
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  758 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-289-112-2

  Query Match             31.5%;  Score 1248.5;  DB 1;  Length 758;
  Best Local Similarity   37.9%;  Pred. No. 4.4e-114;
  Matches  282;  Conservative  121;  Mismatches  281;  Indels   61;  Gaps   21;

Qy      23 LVVFVGGTLVLGTILFLVSQGLLSLQAKQEYCLKPECIEAAAAILSKVNLSVDPCDNFFR 82
           ||| |   |    :  |   |:          ||   ||   ::||| :: :|||| :||
Db      57 LVVLV-ALLAAALVACLAVLGIQYQTRTPSVCLSEGCISVTSSILSSMDPTVDPCQDFFT 115

Qy      83 FACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLEKSISRRRDTEAIQKAKILYSSC 142
           :|| |||  ||:|:    :| :  |  :    :| ||| | :    :|| :||:: | :|
Db     116 YACGGWIKANPVPDGHSRWGTFSNLWEHNQAIIKHLLENSTA--SVSEAERKAQVYYRAC 173

Qy     143 MNEKAIEKADAKPLLHILRHSPFRWPVLESNIGPEGVWSERKFSLLQTLATFRGQYSNSV 202
           |||  ||:  ||||: ::      |:        | | :  |    ||       |  |
Db     174 MNETRIEELKAKPLMELIEKLG-GWNI-------TGPWDKDNFQ--DTLQVVTSHYHTSP 223

Qy     203 FIRLYVSPDDKASNEHILKLDQATLSLAVREDYLDNSTEAKSYRDALYKFMVDTAVLLGA 262
           |  :||| | | || ::::||: | |  |: || | || :       :||    |||
Db     224 FFSVYVSADSKNSNSNVIQVDQSGLGLPSRDYYL-NKTENEKVLTGYLNYMVQLGKLLGG 282

Qy     263 NS-SRAEHDMKSVLRLEIKIAEIMIPHENRTSEAM-YNKMNISELSAMIPQFDWLGYIKK 320
           :       |: :|  |  :| | || | |  | : |:|:  :||  : |  :|| :
Db     283 GAEDTIRPQMQQILDFETALANITIPQEKRRDEELIYHKVTAAELQTLAPAINWLPF--- 339

Qy     321 VIDTRLYPHLKDISPSENVVVRVPQYFKDLFRILGSERKKTIANYLVWRMVYSRIPNLSR 380
           ::|  ||   :|: || :|:  :|   :  :: |  |  : ||::| :|       | :
Db     340 -LNTIFYP--VEINESEPIVIYDKEYLSKVSTLINSTDKCLLNNYMIWNLVRKTSSFLDQ 396

Qy     381 RFQYRWLEFSRVIQGT-TTLLPQWDKCVNFIESALPYVVGKMFVDVYFQEDKKEMMEELV 439
           |||    :|  |: ||  | ||:|  ||:  |: | : :| |||   | || | :  |::
Db     397 RFQDADEKFMEVMYGTKKTCLPRWKFCVSDTENTLGFALGPMFVKATFAEDSKNIASEII 456

Qy     440 EGVRWAFIDMLEKENEWMDAGTKRKAKEKARAVLAKVGYPEFIM---------NDTHVNE 490
             :: || : |    :|||  |:: ||||| |:   :||| |||          ||
Db     457 LEIKKAFEESL-STLKWMDEDTRKSAKEKADAIYNMIGYPNFIMDPKELDKVFNDYTAVP 515

Qy     491 DLKAIKFSEADYFGNVLQTRKYLAQSDFFW------LRKAVPKTEWFTNPTTVNAFYSAS 544
           ||          || | ::       :| |      ||||  : :|   |  |||:|| :
Db     516 DL---------YFENAMRF------FNFSWRVTADQLRKAPNRDQWSMTPPMVNAYYSPT 560

Qy     545 TNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNGRKYDKNGNLDPWWS 604
           |:| |||| || ||:  :  | :|::| |||:|||| || ||: ||:|||:||| |||
Db     561 KNEIVFPAGILQAPFYTRSS-PNALNFGGIGVVVGHELTHAFDDQGREYDKDGNLRPWWK 619

Qy     605 TESEEKFKEKTKCMINQYSNYYWKKAGLNVKGKRTLGENIADNGGLREAFRAYRKWINDR 664
             | | ||::| ||: || ||      |  | |: ||||||||||||: |:|||: |:  :
Db     620 NSSVEAFKQQTACMVEQYGNY--SVNGEPVNGRHTLGENIADNGGLKAAYRAYQNWV--K 675

Qy     665 RQGLEEPLLPGITFTNNQLFFLSYAHVRCNSYRPEAAREQVQIGAHSPPQFRVNGAISNS 724
           : | |:  || :  ||||||||||:  | |:   ||:: | :    ||| :||| |:||||
Db     676 KNGAEQ-TLPTLGLTNNQLFFLSFGQVWCSVRTPESSHEGLITDPHSPSRFRVIGSISNS 734

Qy     725 EEFQKAFNCPPNSTMNRGMDSCRLW 749
           :|| : |:||| | ||      | :|
Db     735 KEFSEHFHCPPGSPMN-PHHKCEVW 758


RESULT 4
US-08-646-273-23
; Sequence 23, Application US/08646273
; Patent No. 6066502
;  GENERAL INFORMATION:
;    APPLICANT:  Kroeger, Burkhard, Seulberger, Harald, Meyer, Thomas, Schmidt,
;    APPLICANT:  Martin, Jacob, Elard, Otter, Rainer, Subkowski, Thomas, Hillen, Hein
;    TITLE OF INVENTION:  Endothelin Converting Enzyme (ECE).
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Keil & Weinkauf
;      STREET:  1101 Connecticut Avenue
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 1.4 Mb storage
;      COMPUTER:  IBM AT-compatible, 80486 processor
;      OPERATING SYSTEM:  MS-DOS version 6.0
;      SOFTWARE:  WordPerfect version 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/646,273
;      FILING DATE:  16-NOV-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/EP94/03706
;      FILING DATE:  11-NOV-1994
;  INFORMATION FOR SEQ ID NO:  23:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  708 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-646-273-23

  Query Match             31.4%;  Score 1241.5;  DB 3;  Length 708;
  Best Local Similarity   37.9%;  Pred. No. 1.9e-113;
  Matches  282;  Conservative  120;  Mismatches  282;  Indels   61;  Gaps   21;

Qy      23 LVVFVGGTLVLGTILFLVSQGLLSLQAKQEYCLKPECIEAAAAILSKVNLSVDPCDNFFR 82
           ||| |   |    :  |   |:          ||   ||   ::||| :: :|||| :||
Db      7 LVVLV-ALLAAALVACLAVLGIQYQTRTPSVCLSEACISVTSSILSSMDPTVDPCQDFFT 65

Qy      83 FACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLEKSISRRRDTEAIQKAKILYSSC 142
           :|| |||  ||:|:    :| :  |  :    :| ||| | :    :|| :| :  | :|
Db      66 YACGGWIKANPVPDGHSRWGTFSNLWEHNQAIIKHLLENSTA--SVSEAERKDQEYYRAC 123

Qy     143 MNEKAIEKADAKPLLHILRHSPFRWPVLESNIGPEGVWSERKFSLLQTLATFRGQYSNSV 202
           |||  ||:  ||||: ::      | :       | | :  |    ||       |  |
Db     124 MNETRIEELKAKPLMELIEKLG-GWNI-------TGPWDKDNFQ--DTLQVVTSHYHTSP 173

Qy     203 FIRLYVSPDDKASNEHILKLDQATLSLAVREDYLDNSTEAKSYRDALYKFMVDTAVLLGA 262
           |  :||| | | || ::::||: | |  |: || | || :       :||    |||
Db     174 FFSVYVSADSKNSNSNVIQVDQSGLGLPSRDYYL-NKTENEKVLTGYLNYMVQLGKLLGG 232
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Qy    263 NS-SRAEHDMKSVLRLEIKIAEIMIPHENRTSEAM-YNKMNISELSAMIPQFDWLGYIKK 320
          :       |: :|  |  :| | || | |  | : |:|:  :||  : |  :|| :
Db    233 GAEDTIRPQMQQILDFETALANITIPQEKRRDEELIYHKVTAAELQTLAPAINWLPF--- 289

Qy    321 VIDTRLYPHLKDISPSENVVVRVPQYFKDLFRILGSERKKTIANYLVWRMVYSRIPNLSR 380
           ::|  ||   :|: || :|:   :|   :  :: |  |  : ||::| :|      | :
Db    290 -LNTIFYP--VEINESEPIVIYDKEYLSKVSTLINSTDKCLLNNYMIWNLVRKTSSFLDQ 346

Qy    381 RFQYRWLEFSRVIQGT-TTLLPQWDKCVNFIESALPYVVGKMFVDVYFQEDKKEMMEELV 439
          |||    :|  |: ||  | ||:|  ||:  |: | : :| |||   | || | :  |::
Db    347 RFQDADEKFMEVMYGTKKTCLPRWKFCVSDTENTLGFALGPMFVKATFAEDSKNIASEII 406

Qy    440 EGVRWAFIDMLEKENEWMDAGTKRKAKEKARAVLAKVGYPEFIM---------NDTHVNE 490
            :: || : |    :|||  |:: ||||| |:   :||| |||          ||
Db    407 LEIKKAFEESL-STLKWMDEDTRKSAKEKADAIYNMIGYPNFIMDPKELDKVFNDYTAVP 465

Qy    491 DLKAIKFSEADYFGNVLQTRKYLAQSDFFW------LRKAVPKTEWFTNPTTVNAFYSAS 544
          ||         || | ::        :| |      |||| : :|   |  |||:|| :
Db    466 DL---------YFENAMRF------FNFSWRVTADQLRKAPNRDQWSMTPPMVNAYYSPT 510

Qy    545 TNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNGRKYDKNGNLDPWWS 604
           |:| |||| || ||:  :  | :|::| |||:|||| || ||: ||:|||:||| |||
Db    511 KNEIVFPAGILQAPFYTRSS-PNALNFGGIGVVVGHELTHAFDDQGREYDKDGNLRPWWK 569

Qy    605 TESEEKFKEKTKCMINQYSNYYWKKAGLNVKGKRTLGENIADNGGLREAFRAYRKWINDR 664
            | | ||::| ||: || ||      |  | |: |||||||||||: |:|||: |:  :
Db    570 NSSVEAFKQQTACMVEQYGNY--SVNGEPVNGRHTLGENIADNGGLKAAYRAYQNWV--K 625

Qy    665 RQGLEEPLLPGITFTNNQLFFLSYAHVRCNSYRPEAAREQVQIGAHSPPQFRVNGAISNS 724
          : | |:  || :  ||||||||||:| | |:   ||:: | :    ||| :||| |:|||
Db    626 KNGAEQ-TLPTLGLTNNQLFFLSFAQVWCSVRTPESSHEGLITDPHSPSRFRVIGSISNS 684

Qy    725 EEFQKAFNCPPNSTMNRGMDSCRLW 749
          :|| : |:||| | ||     | :|
Db    685 KEFSEHFHCPPGSPMN-PHHKCEVW 708
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RESULT 5
US-08-646-273-30
; Sequence 30, Application US/08646273
; Patent No. 6066502
; GENERAL INFORMATION:
; APPLICANT: Kroeger, Burkhard, Seulberger, Harald, Meyer, Thomas, Schmidt,
; APPLICANT: Martin, Jacob, Elard, Otter, Rainer, Subkowski, Thomas, Hillen, Heinz.
; TITLE OF INVENTION: Endothelin Converting Enzyme (ECE).
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Keil & Weinkauf
; STREET: 1101 Connecticut Avenue
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
; COMPUTER: IBM AT-compatible, 80486 processor
; OPERATING SYSTEM: MS-DOS version 6.0
; SOFTWARE: WordPerfect version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,273
; FILING DATE: 16-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP94/03706
; FILING DATE: 11-NOV-1994
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 754 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-646-273-30

Query Match 31.4%; Score 1241.5; DB 3; Length 754;
Best Local Similarity 37.9%; Pred. No. 2.2e-113;
Matches 282; Conservative 120; Mismatches 282; Indels 61; Gaps 21;

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Qy     23 LVVFVGGTLVLGTILFLVSQGLLSLQAKQEYCLKPECIEAAAAILSKVNLSVDPCDNFFR 82
          ||| |   |    :  |   |:          ||   ||   ::||| :: :|||| :||
Db     53 LVVLV-ALLAAALVACLAVLGIQYQTRTPSVCLSEACISVTSSILSSMDPTVDPCQDFFT 111

Qy     83 FACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLEKSISRRRDTEAIQKAKILYSSC 142
          :|| ||| |||:|:    :|  :  |  :    :| ||| | :    :|| :| :  | :|
Db    112 YACGGWIKANPVPDGHSRWGTFSNLWEHNQAIIKHLLENSTA--SVSEAERKDQEYYRAC 169

Qy    143 MNEKAIEKADAKPLLHILRHSPFRWPVLESNIGPEGVWSERKFSLLQTLATFRGQYSNSV 202
          |||  ||:  |||| :: |  :        | | :  |    ||      |  |
Db    170 MNETRIEELKAKPLMELIEKLG-GWNI-------TGPWDKDNFQ--DTLQVVTSHYHTSP 219

Qy    203 FIRLYVSPDDKASNEHILKLDQATLSLAVREDYLDNSTEAKSYRDALYKFMVDTAVLLGA 262
          |  :||| | | || ::::::||: | |  |: || | || :        :||    |||
Db    220 FFSVYVSADSKNSNSNVIQVDQSGLGLPSRDYYL-NKTENEKVLTGYLNYMVQLGKLLGG 278

Qy    263 NS-SRAEHDMKSVLRLEIKIAEIMIPHENRTSEAM-YNKMNISELSAMIPQFDWLGYIKK 320
          :       |: :|  |  :| | || | |  | : |:|:  :||  : |  :|| :
Db    279 GAEDTIRPQMQQILDFETALANITIPQEKRRDEELIYHKVTAAELQTLAPAINWLPF--- 335

Qy    321 VIDTRLYPHLKDISPSENVVVRVPQYFKDLFRILGSERKKTIANYLVWRMVYSRIPNLSR 380
           ::|  ||   :|: || :|:   :|   :  :: |  |  : ||::| :|      | :
Db    336 -LNTIFYP--VEINESEPIVIYDKEYLSKVSTLINSTDKCLLNNYMIWNLVRKTSSFLDQ 392

Qy    381 RFQYRWLEFSRVIQGT-TTLLPQWDKCVNFIESALPYVVGKMFVDVYFQEDKKEMMEELV 439
          |||    :|  |: ||  | ||:|  ||:  |: | : :| |||    | || | :  |::
Db    393 RFQDADEKFMEVMYGTKKTCLPRWKFCVSDTENTLGFALGPMFVKATFAEDSKNIASEII 452

Qy    440 EGVRWAFIDMLEKENEWMDAGTKRKAKEKARAVLAKVGYPEFIM---------NDTHVNE 490
            :: || : |    :|||  |:: ||||| |:   :||| |||          ||
Db    453 LEIKKAFEESL-STLKWMDEDTRKSAKEKADAIYNMIGYPNFIMDPKELDKVFNDYTAVP 511

Qy    491 DLKAIKFSEADYFGNVLQTRKYLAQSDFFW------LRKAVPKTEWFTNPTTVNAFYSAS 544
          ||         || | ::        :| |      |||| : :|   |  |||:|| :
Db    512 DL---------YFENAMRF------FNFSWRVTADQLRKAPNRDQWSMTPPMVNAYYSPT 556

Qy    545 TNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNGRKYDKNGNLDPWWS 604
           |:| |||| || ||:  :  | :|::| |||:|||| || ||: ||:|||:||| |||
Db    557 KNEIVFPAGILQAPFYTRSS-PNALNFGGIGVVVGHELTHAFDDQGREYDKDGNLRPWWK 615

Qy    605 TESEEKFKEKTKCMINQYSNYYWKKAGLNVKGKRTLGENIADNGGLREAFRAYRKWINDR 664
            | | ||::| ||: || ||      |  | |: |||||||||||: |:|||: |:  :
Db    616 NSSVEAFKQQTACMVEQYGNY--SVNGEPVNGRHTLGENIADNGGLKAAYRAYQNWV--K 671

Qy    665 RQGLEEPLLPGITFTNNQLFFLSYAHVRCNSYRPEAAREQVQIGAHSPPQFRVNGAISNS 724
          : | |:  || :  ||||||||||:| | |:   ||:: | :    ||| :||| |:|||
Db    672 KNGAEQ-TLPTLGLTNNQLFFLSFAQVWCSVRTPESSHEGLITDPHSPSRFRVIGSISNS 730

Qy    725 EEFQKAFNCPPNSTMNRGMDSCRLW 749
          :|| : |:||| | ||     | :|
Db    731 KEFSEHFHCPPGSPMN-PHHKCEVW 754
```

RESULT 6
US-08-574-763-2
; Sequence 2, Application US/08574763
; Patent No. 5736376
; GENERAL INFORMATION:
; APPLICANT: Yanagisawa, Masashi
; TITLE OF INVENTION: RECOMBINANT ENDOTHELIN CONVERTING
; TITLE OF INVENTION: ENZYME-2 AND ITS USE IN ECE INHIBITOR SCREENING
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433

```
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/574,763
;      FILING DATE:  Concurrently herewith
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Corder, Timothy S.
;      REGISTRATION NUMBER:  38,414
;      REFERENCE/DOCKET NUMBER:  UTXD:472
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (512) 418-3000
;      TELEFAX:  (512) 474-7577
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  787 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-08-574-763-2

  Query Match             29.9%;  Score 1184;  DB 1;  Length 787;
  Best Local Similarity   35.1%;  Pred. No. 1.1e-107;
  Matches  265;  Conservative  138;  Mismatches  313;  Indels   38;  Gaps   18;

Qy       4 ETGSSVETGKKANRGTRIALVVFVGGTLVLGTILF--LVSQGL-LSLQAKQEYCLKPECI 60
Db      64 EAGFRKRTSRLLGLHTQLELVL-AGVSLLLAALLLGCLVALGVQYHRDPSHSTCLTEACI 122

Qy      61 EAAAAILSKVNLSVDPCDNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLE 120
Db     123 RVAGKILESLDRGVSPCEDFYQFSCGGWIRRNPLPDGRSRWNNSNSLWDQNQAILKHLLE 182

Qy     121 KSISRRRDTEAIQKAKILYSSCMNEKAIEKADAKPLLHILRHSPFRWPVLESNIG---PE 177
Db     183 NT-TFNSSSEAERKTQRFYLSCLQVERIEELGA----HALRD-------LIDKIGGWNVT 230

Qy     178 GVWSERKFSLLQTLATFRGQYSNSVFIRLYVSPDDKASNEHILKLDQATLSLAVREDYLD 237
Db     231 GPWDQDNF--MEVLKAVAGTYRATPFFTVYVSADSKSSNSNIIQVDQSGLFLPSRDYYL- 287

Qy     238 NSTEAKSYRDALYKFMVDTAVLLGANSSRAEHDMKSVLRLEIKIAEIMIPH-ENRTSEAM 296
Db     288 NRTANEKVLTAYLDYMEELGMLLGGQPTSTREQMRQVLELEIQLANITVPQDQRRDEEKI 347

Qy     297 YNKMNISELSAMIPQFDWLGYIKKVIDTRLYPHLKDISPSENVVVRVPQYFKDLFRILGS 356
Db     348 YHKMSIAELQALAPSMDWLEFLSFLLSP------LELGDSEPVVVYGTDYLQQVSELINR 401

Qy     357 ERKKTIANYLVWRMVYSRIPNLSRRFQYRWLEFSRVIQGT-TTLLPQWDKCVNFIESALP 415
Db     402 TEPSVLNNYLIWNLVQKTTSSLDHRFESAQEKLLETLYGTKKSCTPRWQTCISNTDDALG 461

Qy     416 YVVGKMFVDVYFQEDKKEMMEELVEGVRWAFIDMLEKENEWMDAGTKRKAKEKARAVLAK 475
Db     462 FALGSLFVKATFDRQSKEIAEGMISEIRVAFEEAL-GHLVWMDEKTRQAAKEKADAIYDM 520

Qy     476 VGYPEFIMNDTHVNEDLKAIKFSEADYFGNVLQTRKYLAQSDFFWLRKAVPKTEWFTNPT 535
Db     521 IGFPDFILEPKELDDVYDGYEVSEDSFFQNMLNLYNFSAKVMADQLRKPPSRDQWSMTPQ 580

Qy     536 TVNAFYSASTNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNGRKYDK 595
Db     581 TVNAYYLPTKNEIVFPAGILQAPFY-TCNHPQALNFGGIGVVMGHELTHAFDDQGREYDK 639

Qy     596 NGNLDPWWSTESEEKFKEKTKCMINQYSNYYWKKAGLNVKGKRTLGENIADNGGLREAFR 655
Db     640 EGNLRPWWQNESLAAFRNHTACIEEQYSQY--QVNGEKLNGRQTLGENIADNGGLKAAYN 697

Qy     656 AYRKWINDRRQGLEEPLLPGITFTNNQLFFLSYAHVRCNSYRPEAAREQVQIGAHSPPQF 715
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Db     698 AYKAWL--RKHG-EEQQLPAVGLTNHQLFFVGFAQVWCSVRTPESSHEGLVTDPHSPARF 754

Qy     716 RVNGAISNSEEFQKAFNCPPNSTMNRGMDSCRLW 749
Db     755 RVLGTLSNSRDFLRHFGCPVGSPMNSG-QLCEVW 787


RESULT 7
US-09-305-640-2
; Sequence 2,.Application US/09305640B
; Patent No. 6255468
; GENERAL INFORMATION:
;  APPLICANT: SmithKline Beecham plc
;  TITLE OF INVENTION: No. 6255468el Compounds
;  FILE REFERENCE: GP30124
;  CURRENT APPLICATION NUMBER: US/09/305,640B
;  CURRENT FILING DATE: 1999-05-05
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
;   LENGTH: 775
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-305-640-2

  Query Match             24.8%;  Score 983.5;  DB 4;  Length 775;
  Best Local Similarity   31.0%;  Pred. No. 6.8e-88;
  Matches  233;  Conservative  158;  Mismatches  294;  Indels   67;  Gaps   19;

Qy      23 LVVFVGGTLVLGTILFLVSQGLLSL--QAKQEYCLKPECIEAAAAIL-SKVNLSVDPCDN 79
Db      66 LVFAAGLCAILAAMLALKYLGPVAAGGGACPEGCPERKAFARAARFLAANLDASIDPCQD 125

Qy      80 FFRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLEKSISRRRDTEAIQKAKILY 139
Db     126 FYSFACGGWLRRHAIPDDKLTYGTIAAIGEQNEERLRRLLARP-GGGPGGAAQRKVRAFF 184

Qy     140 SSCMNEKAIEKADAKPLLHILRHSPFRWPVLESNIGPEGVW-----SER-----KFSLLQ 189
Db     185 RSCLDMREIERLGPRPMLEVIEDC-------------GGWDLGGAEERPGVAARWDLNR 230

Qy     190 TLATFRGQYSNSVFIRLYVSPDDKASNEHILKLDQATLSLAVREDYLDNSTEAKSYRDAL 249
Db     231 LLYKAQGVYSAAALFSLTVSLDDRNSSRYVIRIDQDGLTLPERTLYLAQDEDSEKILAAY 290

Qy     250 YKFMVDTAVLLGANSSRAEHDMKSVLRLEIKIAEIMIPHEN---RTSEAMYNKMNISELS 306
Db     291 RVFMERVLSLLGADA--VEQKAQEILQVEQQLANITVSEYDDLRRDVSSMYNKVTLGQLQ 348

Qy     307 AMIPQFDWLGYIKKVIDTRLYPHLKDISPSENVVVRVPQYFKDLFRILGSERKKTIANYL 366
Db     349 KITPHLRWKWLLDQIFQ-------EDFSEEEEVVLLATDYMQQVSQLIRSTPHRVLHNYL 401

Qy     367 VWRMVYSRIPNLSRRFQYRWLEFSRVIQGTTTLLPQWDK-------CVNFIESALPYVVG 419
Db     402 VWRVVVVLSEHLSPPFREALHELAQEMEGS-------DKPQELARVCLGQANRHFGMALG 454

Qy     420 KMFVDVYFQEDKKEMMEELVEGVRWAFIDMLEKENEWMDAGTKRKAKEKARAVLAKVGYP 479
Db     455 ALFVHEHFSAASKAKVQQLVEDIKYILGQRLE-ELDWMDAETRAAARAKLQYMMVMVGYP 513

Qy     480 EFIMNDTHVNEDLKAIKFSEADYFGNVLQTRKYLAQSDFFWLRKAVPKTEWFTNPTTVNA 539
Db     514 DFLLKPDAVDKEYE-FEVHEKTYFKNILNSIRFSIQLSVKKIRQEVDKSTWLLPPQALNA 572

Qy     540 FYSASTNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNGRKYDKNGNL 599
Db     573 YYLPNKNQMVFPAGILQ-PTLYDPDFPQSLNYGGIGTIIGHELTHGYDDWGGQYDRSGNL 631

Qy     600 DPWWSTESEEKFKEKTKCMINQYSNY--YWKKAGLNVKGKRTLGENIADNGGLREAFRAY 657
Db     632 LHWWTEASYSRFLRKAECIVRLYDNFTVYNQR----VNGKHTLGENIADMGGLKLAYHAY 687
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Qy     658 RKWINDRRQGLEEPLLPGITFTNNQLFFLSYAHVRCNSYRPEAAREQVQIGAHSPPQFRV 717
           :||:  |  | | | || : :|::||||:::|   |   | ::   ||    |:|  :||
Db     688 QKWV--REHGPEHP-LPRLKYTHDQLFFIAFAQNWCIKRRSQSIYLQVLTDKHAPEHYRV 744

Qy     718 NGAISNSEEFQKAFNCPPNSTMNRGMDSCRLW 749
           |::|  ||| :||:|| :| ||     | :|
Db     745 LGSVSQFEEFGRAFHCPKDSPMNPA-HKCSVW 775


RESULT 8
US-08-646-273-19
; Sequence 19, Application US/08646273
; Patent No. 6066502
;  GENERAL INFORMATION:
;    APPLICANT:  Kroeger, Burkhard, Seulberger, Harald, Meyer, Thomas, Schmidt,
;    APPLICANT:  Martin, Jacob, Elard, Otter, Rainer, Subkowski, Thomas, Hillen, Heinz.
;    TITLE OF INVENTION:  Endothelin Converting Enzyme (ECE).
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Keil & Weinkauf
;      STREET:  1101 Connecticut Avenue
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 1.4 Mb storage
;      COMPUTER:  IBM AT-compatible, 80486 processor
;      OPERATING SYSTEM:  MS-DOS version 6.0
;      SOFTWARE:  WordPerfect version 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/646,273
;      FILING DATE:  16-NOV-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/EP94/03706
;      FILING DATE:  11-NOV-1994
;  INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  567 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-646-273-19

  Query Match             24.3%;  Score 963.5;  DB 3;  Length 567;
  Best Local Similarity   37.7%;  Pred. No. 3.8e-86;
  Matches  226;  Conservative   96;  Mismatches  216;  Indels   61;  Gaps   21;

Qy     106 WLRHNVDLKLKELLEKSISRRRDTEAIQKAKILYSSCMNEKAIEKADAKPLLHILRHSPF 165
           |  ||  : :| ||| | :    :|| :| :  | :||||  ||:  ||||: ::
Db      12 W-EHNQAI-IKHLLENSTA--SVSEAERKDQEYYRACMNETRIEELKAKPLMELIEKLG- 66

Qy     166 RWPVLESNIGPEGVWSERKFSLLQTLATFRGQYSNSVFIRLYVSPDDKASNEHILKLDQA 225
           | :       | | :  |    ||      |  | |  :||| | | || :::::||:
Db      67 GWNI-------TGPWDKDNFQ--DTLQVVTSHYHTSPFFSVYVSADSKNSNSNVIQVDQS 117

Qy     226 TLSLAVREDYLDNSTEAKSYRDALYKFMVDTAVLLGANS-SRAEHDMKSVLRLEIKIAEI 284
           | |  |: || | || :        :||    |||  :       |: :|  |  :| |
Db     118 GLGLPSRDYYL-NKTENEKVLTGYLNYMVQLGKLLGGGAEDTIRPQMQQILDFETALANI 176

Qy     285 MIPHENRTSEAM-YNKMNISELSAMIPQFDWLGYIKKVIDTRLYPHLKDISPSENVVVRV 343
           || | |  | : |:|:  :|| : |  :|| :    ::|  ||   :|: || :|:
Db     177 TIPQEKRRDEELIYHKVTAAELQTLAPAINWLPF----LNTIFYP--VEINESEPIVIYD 230

Qy     344 PQYFKDLFRILGSERKKTIANYLVWRMVYSRIPNLSRRFQYRWLEFSRVIQGT-TTLLPQ 402
           :|   :  :: |  |  : ||::| :|      | :|||    :|  |: ||  | ||:
Db     231 KEYLSKVSTLINSTDKCLLNNYMIWNLVRKTSSFLDQRFQDADEKFMEVMYGTKKTCLPR 290

Qy     403 WDKCVNFIESALPYVVGKMFVDVYFQEDKKEMMEELVEGVRWAFIDMLEKENEWMDAGTK 462
           |  ||:  |: | : :| |||   | || | :  |::  :: || : |    :|||  |:
Db     291 WKFCVSDTENTLGFALGPMFVKATFAEDSKNIASEIILEIKKAFEESL-STLKWMDEDTR 349

Qy     463 RKAKEKARAVLAKVGYPEFIM---------NDTHVNEDLKAIKFSEADYFGNVLQTRKYL 513
           : ||||| |:   :||| |||          ||      ||          || | ::
Db     350 KSAKEKADAIYNMIGYPNFIMDPKELDKVFNDYTAVPDL---------YFENAMRF---- 396

Qy     514 AQSDFFW------LRKAVPKTEWFTNPTTVNAFYSASTNQIRFPAGELQKPFFWGTEYPR 567
           :| |       ||||  : :|   |  |||:|| : |:| |||| || ||:  :  |
Db     397 --FNFSWRVTADQLRKAPNRDQWSMTPPMVNAYYSPTKNEIVFPAGILQAPFYTRSS-PN 453

Qy     568 SLSYGAIGVIVGHEFTHGFDNNGRKYDKNGNLDPWWSTESEEKFKEKTKCMINQYSNYYW 627
           :|::| |||:|||| || ||: ||:|||:||| |||   | | ||::| ||: || ||
Db     454 ALNFGGIGVVVGHELTHAFDDQGREYDKDGNLRPWWKNSSVEAFKQQTACMVEQYGNY-- 511

Qy     628 KKAGLNVKGKRTLGENIADNGGLREAFRAYRKWINDRRQGLEEPLLPGITFTNNQLFFL 686
           |  | |: ||||||||||||: |:|||: |:  :: | |:  || :  ||||||||
Db     512 SVNGEPVNGRHTLGENIADNGGLKAAYRAYQNWV--KKNGAEQ-TLPTLGLTNNQLFFL 567


RESULT 9
US-08-646-273-14
; Sequence 14, Application US/08646273
; Patent No. 6066502
;  GENERAL INFORMATION:
;    APPLICANT:  Kroeger, Burkhard, Seulberger, Harald, Meyer, Thomas, Schmidt,
;    APPLICANT:  Martin, Jacob, Elard, Otter, Rainer, Subkowski, Thomas, Hillen, Hein
;    TITLE OF INVENTION:  Endothelin Converting Enzyme (ECE).
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Keil & Weinkauf
;      STREET:  1101 Connecticut Avenue
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 1.4 Mb storage
;      COMPUTER:  IBM AT-compatible, 80486 processor
;      OPERATING SYSTEM:  MS-DOS version 6.0
;      SOFTWARE:  WordPerfect version 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/646,273
;      FILING DATE:  16-NOV-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/EP94/03706
;      FILING DATE:  11-NOV-1994
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  189 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-646-273-14

  Query Match             13.3%;  Score 527.5;  DB 3;  Length 189;
  Best Local Similarity   51.8%;  Pred. No. 6.6e-44;
  Matches  101;  Conservative   32;  Mismatches   55;  Indels    7;  Gaps    5;

Qy     555 LQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNGRKYDKNGNLDPWWSTESEEKFKEK 614
           || ||:  :  | :|::| |||:|||| || ||: ||:|||:||| |||   | | ||::
Db       2 LQAPFYTRSS-PNALNFGGIGVVVGHELTHAFDDQGREYDKDGNLRPWWKNSSVEAFKQQ 60

Qy     615 TKCMINQYSNYYWKKAGLNVKGKRTLGENIADNGGLREAFRAYRKWINDRRQGLEEPLLP 674
           | ||: || ||     |  | |: ||||||||||||: |:|||: |:  :: | |:  ||
Db      61 TACMVEQYGNY--SVNGEPVNGRHTLGENIADNGGLKAAYRAYQNWV--KKNGAEQ-TLP 115

Qy     675 GITFTNNQLFFLSYAHVRCNSYRPEAAREQVQIGAHSPPQFRVNGAISNSEEFQKAFNCP 734
           :  ||||||||:| | |:   ||:: | :    ||| :||| |:|||:|| : |:||
Db     116 TLGLTNNQLFFLSFAQVWCSVRTPESSHEGLITDPHSPSRFRVIGSISNSKEFSEHFHCP 175

Qy     735 PNSTMNRGMDSCRLW 749
           | | ||     | :|
Db     176 PGSPMN-PHHKCEVW 189
```

```
RESULT 10
US-09-305-640-4
; Sequence 4, Application US/09305640B
; Patent No. 6255468
; GENERAL INFORMATION:
;  APPLICANT: SmithKline Beecham plc
;  TITLE OF INVENTION: No. 6255468el Compounds
;  FILE REFERENCE: GP30124
;  CURRENT APPLICATION NUMBER: US/09/305,640B
;  CURRENT FILING DATE: 1999-05-05
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
;   LENGTH: 181
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: UNSURE
;   LOCATION: (134)(145)(162)
US-09-305-640-4

  Query Match             6.2%;  Score 246;  DB 4;  Length 181;
  Best Local Similarity   32.6%;  Pred. No. 3.9e-16;
  Matches   62;  Conservative   36;  Mismatches   76;  Indels   16;  Gaps    5;

Qy    476 VGYPEFIMNDTHVNEDLKAIKFSEADYFGNVLQTRKYLAQSDFFWLRKAVPKTEWFTNPT 535
Db      1 VGYPDFLLKPDAVDKEYE-FEVHEKTYFKNILNSIRFSIQLSVKKIRQEVDKSTWLLPPQ 59

Qy    536 TVNAFYSASTNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNG----- 590
Db     60 ALNAYYLPNKNQMVFPAGILQ-PTLYDPDFPQSLNYGGIGTIIGHELTHGYDGLGGPVPL 118

Qy    591 RKYDKNGNLDPWWSTESEEKFKEKTKCMINQYSNYYWKKAGLNVKGKR--TLGENIADNG 648
Db    119 REPACTGGTEASLQPXSCERLSASFPXLWTTFN-------VLQPGGERETXVWENIAVWG 171

Qy    649 GLREAFRAYR 658
Db    172 GLKLAYHAIR 181


RESULT 11
US-08-813-940-25
; Sequence 25, Application US/08813940
; Patent No. 5834279
;  GENERAL INFORMATION:
;    APPLICANT:  Rubin, Harvey
;    APPLICANT:  Yang, Fude
;    APPLICANT:  Avarbock, David
;    APPLICANT:  Curran, Sean
;    TITLE OF INVENTION:  Methods of Identifying Compounds that
;    TITLE OF INVENTION:  Inhibit DNA Synthesis in Mycobacterium Tuberculosis and
;    TITLE OF INVENTION:  Composition, Reagents and Kits for Performing the Same
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Woodcock Washburn Kurtz Mackiewicz & No. 5834279ris
;      STREET:  One Liberty Place, 46th Floor
;      CITY:  Philadelphia
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Windows
;      SOFTWARE:  Wordperfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/813,940
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/612,271
;      FILING DATE:  07-MAR-1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DeLuca, Mark
;      REGISTRATION NUMBER:  33,229
;      REFERENCE/DOCKET NUMBER:  UPAP-0220
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-568-3100
;      TELEFAX:  215-568-3439
;  INFORMATION FOR SEQ ID NO:  25:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  725 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-813-940-25

  Query Match             2.9%;  Score 116;  DB 2;  Length 725;
  Best Local Similarity   19.5%;  Pred. No. 0.029;
  Matches  139;  Conservative  113;  Mismatches  242;  Indels  218;  Gaps   37;

Qy    109 HNVDLKLKELLEKSISRRRDTEAIQKAKILYSSCMNEKAIEKADAKPLLHILRHSPFRWP 168
Db     68 HNQDEKLDYLIRENYYER---EVLDQ----YSRNFVKTLLDRAYAK---------KFRFP 111

Qy    169 VLESNIGPEGVWSERKFSLLQTLATFRGQ------YSNSVFIRLYVSPDDKASNEHILKL 222
Db    112 TFLGAF---------KYYTSYTLKTFDGKRYLERFEDRVVMVALTLAAGDTALAELLV-- 160

Qy    223 DQATLSLAVREDYLDNSTEAKSYRDALYKFMVDTAVLLGA-NSSRAEHDMKSVLRLEIKI 281
Db    161 ----------DEIIDG------------RFQPATPTFLNSGKKQRGEPVSCFLLRVEDNM 198

Qy    282 AEIMIPHENRTSEAMYNKMNISELSAMIPQFDWLGYIKKVIDTRLYPH---LKDISPSEN 338
Db    199 ESI--------GRSINSALQLSKRGGGV----------ALLLTNIREHGGAIKNIENQSS 240

Qy    339 VVVRVPQYFKDLFRI---LGSERKKTIANYL------VWRMVYSRIPNLSRRFQYRWLEF 389
Db    241 GVIPIMKLLEDAFSYANQLGA-RQGAGAVYLHAHHPDIYRFLDTKRENADEKIRIKTLSL 299

Qy    390 SRVIQGTTTLLPQWDKCVNFIESALPYVVGKMFVDVYFQEDKKEMMEELVEGVRWAFIDM 449
Db    300 GVVIPDITFELAKRNDDMYLFS---PYDV-----------------ERVYGVPFADISV 338

Qy    450 LEKENEWMDAGTKRKAKEKAR---AVLAKV----GYPEFIMND-----------TH--- 487
Db    339 TEKYYEMVDDARIRKTKIKAREFFQTLAELQFESGYPYIMFEDTVNRANPIDGKITHSNL 398

Qy    488 ------------VNEDLKAIKFSEADYFGNV--LQTRKYLAQSDF-----FWLR------ 522
Db    399 CSEILQVSTPSLFNEDLSYAKVGK-DISCNLGSLNIAKTMDSPDFAQTIEVAIRALTAVR 457

Qy    523 -----KAVPKTEWFTNPTTVNAFYSASTNQIRFPAGELQKPFFWGTE--------YPRSL 569
Db    458 HQTHIKSVPSIEQGNNDS-----HAIGLGQMNLHGYLARERIFYGSDEGIDFTNIYFYTV 512

Qy    570 SYGAIGV---IVGHEFTH--GFDNNGRKYDKNGNLDPWWSTESEEKFKEKTKCMINQYSN 624
Db    513 LYHALRASNRIAIERGTHFKGFERS--KYASGEFFDKY----TDQIWEPKTQKVRQLFAD 566

Qy    625 YYWKKAGLNVKGKRTLGENIADNGGLREAFRAYRKWINDRRQGLEEPLLPGITFTNNQLF 684
Db    567 -----AGIRIPTQ-------DDWRRLKESVQAH---------GIYNQNLQAVPPTGS--- 602

Qy    685 FLSYAHVRCNSYRPEAAREQV----QIG-AHSPPQFRVNGAISNSEEFQKAF 731
Db    603 -ISYINHSTSSIHPIVSKVEVRKEGKIGRVYYPAPYMTN---DNLEYYEDAY 650


RESULT 12
US-08-392-625-20
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```
; Sequence 20, Application US/08392625
; Patent No. 5837485
;  GENERAL INFORMATION:
;    APPLICANT:  Entian, Karl-Dieter
;    APPLICANT:  G tz, Friedrich
;    APPLICANT:  Schnell, No. 5837485bert
;    APPLICANT:  Augustin, Johannes
;    APPLICANT:  Engelke, Germar
;    APPLICANT:  Rosenstein, Ralf
;    APPLICANT:  Kaletta, Cortina
;    APPLICANT:  Klein, Cora
;    APPLICANT:  Wieland, Bernd
;    APPLICANT:  Kupke, Thomas
;    APPLICANT:  Jung, G nther
;    APPLICANT:  Kellner, Roland
;    TITLE OF INVENTION:  Biosynthetic Process For The Preparation
;    TITLE OF INVENTION:  Of Chemical Compounds
;    NUMBER OF SEQUENCES:  42
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox
;      STREET:  1100 New York Avenue
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/392,625
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/876,791
;      FILING DATE:  30-APR-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Esmond, Robert W.
;      REGISTRATION NUMBER:  32,893
;      REFERENCE/DOCKET NUMBER:  0652.0980002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 371-2600
;      TELEFAX:  (202) 371-2540
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  990 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-08-392-625-20

  Query Match             2.9%;  Score 114.5;  DB 2;  Length 990;
  Best Local Similarity   19.6%;  Pred. No. 0.07;
  Matches  107;  Conservative   92;  Mismatches  199;  Indels  149;  Gaps   30;

Qy    196 GQYSNSVFIRLYVSPDDKASNEHILKLDQATLSLAVREDYLDNSTEAKSYRDAL-----Y 250
          |::| :  |::     | : ::  :|:|   |   |   ||:  ::   |:|:
Db    104 GEFSENNNIKI----KDSSFHKKDVKIDGQWLYKLVH--YLE--SDYTYYKDSFVIWNQQ 155

Qy    251 KFMVDTAVLLGANSSRAEHDMKSVLRLEIKIAEIMIPHENRTSEAMYNKM---------- 300
           :: :  : |  |||  |:    || ::     : | |||      | ::
Db    156 NYIYNNRLYLDNNSSITENKRNDVLSVKYNSILVFI-HENSKKNITYEELVQLISSKYSI 214

Qy    301 -NISELSAMIPQFDWLGYIKKVIDTRLYPHLKDISPSENVVVRVPQYFKDLFRILGSERK 359
           |  |:   : :       |::| : | | |:: :|              |  |: |
Db    215 ENKEEVKVFVQEL----INKEIIFSDLRPTLENKNP-------------LDYIINSLNP 256

Qy    360 KTIANYLVWRMV--------YSRIPNLSRRFQYRWLEFSRVIQGTTTLLPQWDKCVNFIE 411
          |   | ||  ::         ||::|    : :|::|:           |: |     |:::
Db    257 K---NSLVGTLINISNEITKYSKMP--LGKGEYKYLDI-------VNLMSQLFVSKNYLQ 304

Qy    412 SALPYVVGKMFVDVYFQEDKKEMMEELVEGV-RWAFIDMLEKENEWMDAGTKRKAKEKAR 470
                  :| |    : |: : | : :   |:|  |   :|:   |||

Db    305 ----------IDTYIDYSRNELKQSLADNISEAAYILWLLSPHEF---GTKTIR----- 345

Qy    471 AVLAKVGYPEFIMNDTHVNEDLKAIK--FSEADYFGNVLQTRKYLAQSDFFWLRK----A 524
          | || | | :  | |  :|   |: : ||   :   |   ::  :|::     |
Db    346 ------NYHEFFM-DKYGFEQLVNLKQLLSDINGFG-YPKKDSYSFSNNIAFLKEKYLLA 397

Qy    525 VPKTEW--FTNPTTVNAFYSASTNQIRFPAG-ELQKPFFWGTEYPRSLSYGAIGVIVGHE 581
          :      |    |    : : ::|  |   |:    ::|        :  |  |:|
Db    398 IQNNSHIEITENDVKNLEKNNTVSKINAPVSTEIYSEIYFGNSIKGYEDFAVISPILGS- 456

Qy    582 FTHGFDNNGRKYDK-NGNLDPWWSTESEEKFKEKTKCMINQYSNY---------YWKKAG 631
                | |  : :  ||        : :|  :  | ::: |:||            :|
Db    457 -----FNAGATFGRPTGNF-------NIKKKNQLQKEIVHHYNNYMNENDLEISQLNEAP 504

Qy    632 LNVKGKRTLGENIADNGGLREAFRAYRKWINDRRQGLEEP--------LLPGITFTNNQL 683
          || :    | |            | |   :|    | |         :  | ||  |:|
Db    505 LNSRNVNILNNN----------RIYNTCLN-----LNLPKSDIDINDIFIGATF--NKL 546

Qy    684 FFLSYAH 690
          :  |  |
Db    547 YLYSEKH 553


RESULT 13
US-08-466-961A-20
; Sequence 20, Application US/08466961A
; Patent No. 5843709
;  GENERAL INFORMATION:
;    APPLICANT:  Entian, Karl-Dieter
;    APPLICANT:  G tz, Friedrich
;    APPLICANT:  Schnell, No. 5843709bert
;    APPLICANT:  Augustin, Johannes
;    APPLICANT:  Engelke, Germar
;    APPLICANT:  Rosenstein, Ralf
;    APPLICANT:  Kaletta, Cortina
;    APPLICANT:  Klein, Cora
;    APPLICANT:  Wieland, Bernd
;    APPLICANT:  Kupke, Thomas
;    APPLICANT:  Jung, G nther
;    APPLICANT:  Kellner, Roland
;    TITLE OF INVENTION:  Biosynthetic Process for the Preparation of
;    TITLE OF INVENTION:  Chemical Compounds
;    NUMBER OF SEQUENCES:  42
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox
;      STREET:  1100 New York Avenue, NW
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/466,961A
;      FILING DATE:  06-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/392,625
;      FILING DATE:  22-FEB-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/876,791
;      FILING DATE:  30-APR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/784,234
;      FILING DATE:  31-OCT-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Esmond, Robert W.
;      REGISTRATION NUMBER:  32,893
;      REFERENCE/DOCKET NUMBER:  0652.0980004
;    TELECOMMUNICATION INFORMATION:
```

```
;      TELEPHONE:  (202) 371-2600
;      TELEFAX:  (202) 371-2540
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  990 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-08-466-961A-20

  Query Match             2.9%;  Score 114.5;  DB 2;  Length 990;
  Best Local Similarity   19.6%;  Pred. No. 0.07;
  Matches  107;  Conservative   92;  Mismatches  199;  Indels  149;  Gaps   30;

Qy    196 GQYSNSVFIRLYVSPDDKASNEHILKLDQATLSLAVREDYLDNSTEAKSYRDAL-----Y 250
          |::| :  |::     | : ::  :|:|   |   |   ||:  ::   |:|:
Db    104 GEFSENNNIKI----KDSSFHKKDVKIDGQWLYKLVH--YLE--SDYTYYKDSFVIWNQQ 155

Qy    251 KFMVDTAVLLGANSSRAEHDMKSVLRLEIKIAEIMIPHENRTSEAMYNKM---------- 300
           :: :  : |  |||  |:    || ::     : | |||      | ::
Db    156 NYIYNNRLYLDNNSSITENKRNDVLSVKYNSILVFI-HENSKKNITYEELVQLISSKYSI 214

Qy    301 -NISELSAMIPQFDWLGYIKKVIDTRLYPHLKDISPSENVVVRVPQYFKDLFRILGSERK 359
           |  |:   : :       |::| : | | |:: :|              |  |: |
Db    215 ENKEEVKVFVQEL----INKEIIFSDLRPTLENKNP-------------LDYIINSLNP 256

Qy    360 KTIANYLVWRMV--------YSRIPNLSRRFQYRWLEFSRVIQGTTTLLPQWDKCVNFIE 411
          |   | ||  ::        ||::|    : :|::|:          |: |     |:::
Db    257 K---NSLVGTLINISNEITKYSKMP--LGKGEYKYLDI-------VNLMSQLFVSKNYLQ 304

Qy    412 SALPYVVGKMFVDVYFQEDKKEMMEELVEGV-RWAFIDMLEKENEWMDAGTKRKAKEKAR 470
                 :| |    : |: : | : :   |:|  |   :|:  |||
Db    305 ----------IDTYIDYSRNELKQSLADNISEAAYILWLLSPHEF---GTKTIR----- 345

Qy    471 AVLAKVGYPEFIMNDTHVNEDLKAIK--FSEADYFGNVLQTRKYLAQSDFFWLRK----A 524
                | || | | :  | |  :|   |: : ||   :   |   ::  :|::   |
Db    346 ------NYHEFFM-DKYGFEQLVNLKQLLSDINGFG-YPKKDSYSFSNNIAFLKEKYLLA 397

Qy    525 VPKTEW--FTNPTTVNAFYSASTNQIRFPAG-ELQKPFFWGTEYPRSLSYGAIGVIVGHE 581
          :       |     |   : : ::|  |   |:    ::|        :  |  |:|
Db    398 IQNNSHIEITENDVKNLEKNNTVSKINAPVSTEIYSEIYFGNSIKGYEDFAVISPILGS- 456

Qy    582 FTHGFDNNGRKYDK-NGNLDPWWSTESEEKFKEKTKCMINQYSNY---------YWKKAG 631
               | |  : :  ||        : :|  :  | ::: |:||            :|
Db    457 -----FNAGATFGRPTGNF-------NIKKKNQLQKEIVHHYNNYMNENDLEISQLNEAP 504

Qy    632 LNVKGKRTLGENIADNGGLREAFRAYRKWINDRRQGLEEP--------LLPGITFTNNQL 683
          || :    |  |          | |   :|     |  |         :  | ||  |:|
Db    505 LNSRNVNILNNN----------RIYNTCLN-----LNLPKSDIDINDIFIGATF--NKL 546

Qy    684 FFLSYAH 690
          :  |  |
Db    547 YLYSEKH 553


RESULT 14
US-08-645-193B-15
; Sequence 15, Application US/08645193B
; Patent No. 5962253
;  GENERAL INFORMATION:
;    APPLICANT:  Kupke, Thomas
;    APPLICANT:  Gotz, Friedrich
;    APPLICANT:  Kempter, Christoph
;    APPLICANT:  Jung, Gunther
;    TITLE OF INVENTION:  Oxidative Decarboxylation of Peptides
;    TITLE OF INVENTION:  Catalyzed by Flavoprotein EpiD
;    NUMBER OF SEQUENCES:  70
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox P.L.L.C.
;      STREET:  1100 New York Avenue, Suite 600
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/645,193B
;      FILING DATE:  13-MAY-1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Esmond, Robert W.
;      REGISTRATION NUMBER:  32,893
;      REFERENCE/DOCKET NUMBER:  0652.1540000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 371-2600
;      TELEFAX:  (202) 371-2540
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  990 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  protein
US-08-645-193B-15

  Query Match             2.9%;  Score 114.5;  DB 2;  Length 990;
  Best Local Similarity   19.6%;  Pred. No. 0.07;
  Matches  107;  Conservative   91;  Mismatches  200;  Indels  149;  Gaps   30;

Qy    196 GQYSNSVFIRLYVSPDDKASNEHILKLDQATLSLAVREDYLDNSTEAKSYRDAL-----Y 250
          |::| :  |::     | : ::  :|:|   |   |   ||:  ::   |:|:
Db    104 GEFSENNNIKI----KDSSFHKKDVKIDGQWLYKLVH--YLE--SDYTYYKDSFVIWNQQ 155

Qy    251 KFMVDTAVLLGANSSRAEHDMKSVLRLEIKIAEIMIPHENRTSEAMYNKM---------- 300
           :: :  : |  |||  |:    || ::     : | |||      | ::
Db    156 NYIYNNRLYLDNNSSITENKRNDVLSVKYNSILVFI-HENSKKNITYEELVQLISSKYSI 214

Qy    301 -NISELSAMIPQFDWLGYIKKVIDTRLYPHLKDISPSENVVVRVPQYFKDLFRILGSERK 359
           |  |:   : :       |::| : | | |:: :|              |  |: |
Db    215 ENKEEVKVFVQEL----INKEIIFSDLRPTLENKNP-------------LDYIINSLNP 256

Qy    360 KTIANYLVWRMV--------YSRIPNLSRRFQYRWLEFSRVIQGTTTLLPQWDKCVNFIE 411
          |   | ||  ::        ||::|    : :|::|:          |: |     |:::
Db    257 K---NSLVGTLINISNEITKYSKMP--LGKGEYKYLDI-------VNLMSQLFVSKNYLQ 304

Qy    412 SALPYVVGKMFVDVYFQEDKKEMMEELVEGV-RWAFIDMLEKENEWMDAGTKRKAKEKAR 470
                 :| |    : |: : | : :   |:|  |   :|:  |||
Db    305 ----------IDTYIDYSRNELKQSLADNISEAAYILWLLSPNHF---GTKTIR----- 345

Qy    471 AVLAKVGYPEFIMNDTHVNEDLKAIK--FSEADYFGNVLQTRKYLAQSDFFWLRK----A 524
                | || | | :  | |  :|   |: : ||   :   |   ::  :|::   |
Db    346 ------NYHEFFM-DKYGFEQLVNLKQLLSDINGFG-YPKKDSYSFSNNIAFLKEKYLLA 397

Qy    525 VPKTEW--FTNPTTVNAFYSASTNQIRFPAG-ELQKPFFWGTEYPRSLSYGAIGVIVGHE 581
          :       |     |   : : ::|  |   |:    ::|        :  |  |:|
Db    398 IQNNSHIEITENDVKNLEKNNTVSKINAPVSTEIYSEIYFGNSIKGYEDFAVISPILGS- 456

Qy    582 FTHGFDNNGRKYDK-NGNLDPWWSTESEEKFKEKTKCMINQYSNY---------YWKKAG 631
               | |  : :  ||        : :|  :  | ::: |:||            :|
Db    457 -----FNAGATFGRFTGNF-------NIKKKNQLQKEIVHHYNNYMNENDLEISQLNEAP 504

Qy    632 LNVKGKRTLGENIADNGGLREAFRAYRKWINDRRQGLEEP--------LLPGITFTNNQL 683
          || :    |  |          | |   :|     |  |         :  | ||  |:|
Db    505 LNSRNVNILNNN----------RIYNTCLN-----LNLPKSDIDINDIFIGATF--NKL 546

Qy    684 FFLSYAH 690
          :  |  |
Db    547 YLYSEKH 553


RESULT 15
US-08-655-345-4
; Sequence 4, Application US/08655345
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```
; Patent No. 5830742
;  GENERAL INFORMATION:
;    APPLICANT:  Black, Roy A.
;    APPLICANT:  Rauch, Charles
;    APPLICANT:  March, Carl J.
;    APPLICANT:  Cerretti, Douglas P.
;    TITLE OF INVENTION:  TNF-a CONVERTING ENZYME
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Immunex Corporation
;      STREET:  51 University Street
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Macintosh
;      OPERATING SYSTEM:  Apple Operating System 7.5.2
;      SOFTWARE:  Microsoft Word for Apple, Version 6.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/655,345
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/504,614
;      FILING DATE:  20-JUL-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/428,458
;      FILING DATE:  8-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Malaska, Stephen L.
;      REGISTRATION NUMBER:  32,655
;      REFERENCE/DOCKET NUMBER:  2507-B
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 587-0430
;      TELEFAX:  (206) 233-0644
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  681 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-655-345-4

  Query Match             2.7%;  Score 108;  DB 2;  Length 681;
  Best Local Similarity   18.9%;  Pred. No. 0.16;
  Matches  140;  Conservative   96;  Mismatches  237;  Indels  266;  Gaps   38;

Qy      93 PIPEDMPSYGVYPWLRHNVDLKLKELLEKSISRRRDTEAIQKAKILYSSCMNEKAIEKAD 152
           | | | | :| :            : |||  |   | :      ||  | : : :: | |
Db       1 PRPPDDPGFGPH-----------QRLEKLDSLLSDYD------ILSLSNIQQHSVRKRD 42

Qy     153 AKPLLHI---LRHSPFRWPVLESNIGPEGVWSERKFSLLQTLATFRGQYSNSVFIRLYVS 209
           :   |:   | | :                | | |  | :| |   :  |     |
Db      43 LQTSTHVETLLTFSALK---------------RHFKLYLTSSTERFSQNFKV-----VV 81

Qy     210 PDDKASNEHILKLDQATLSLAVREDYLDNSTEAKSYRDALYKFMVDTAVLLGANSSRAEH 269
           | |  :|: :|         | |   |:   |          : |  |::  |:  ||:
Db      82 VDGKNESEYTVKWQDFFTGHVVGEP--DSRVLA---------HIRDDDVIIRINTDGAEY 130

Qy     270 DMKSVLRLEIKIAEIMIPHENRTSE---AMYNKMNISELSAM-IPQFDWLGYIKKVIDTR 325
           ::: : |             | | :    :|   :|  :| :  |:    ||:|   :
Db     131 NIEPLWRF-----------VNDTKDKRMLVYKSEDIKNVSRLQSPKV--CGYLKVDNEEL 177

Qy     326 LYPHLKDISPSENVVVRV-----PQYFKD-----------LFRILGSERKKTIANYLVWR 369
           |   | |  | | :| ||     |   |:           :| :|   : |  |||:
Db     178 LPKGLVDREPPEELVHRVKRRADPDPMKNTCKLLVVADHRFYRYMGRGEESTTTNYLI-- 235

Qy     370 MVYSRIPNLSRRFQYRW-----------LEFSRVIQGTTTLLPQWDKCVNFIESALPYVV 418
           :  |: :: |     |           :|  |:::    : |  :|  |  :|
Db     236 ELIDRVDDIYRNTS--WDNAGFKGYGIQIEQIRILKSPQEVKP-GEKHYNMAKS------ 286

Qy     419 GKMFVDVYFQEDK-----KEMMEELVEGVRWAFIDMLEKENEWMDAGTKRKAKEKARAVL 473
                 |  |:|     | ::|:    :                        |:| ::  |
Db     287 -------YPNEEKDAWDVKMLLEQFSFDI---------------------AEEASKVCL 317

Qy     474 AKV-GYPEFIMNDTHVNEDLKAIKFSEADYFGNVLQTRKYLAQSDFFWLRKAVPKTEWFT 532
           | :  | :| |         |  :    |:  | |                  ||
Db     318 AHLFTYQDFDMGTL----GLAYVGSPRANSHGGV-----------------CPK----- 350

Qy     533 NPTTVNAFYSASTNQIRFPAGELQKPFFWGTEYPRSLSYG------AIGVIVGHEFTHGF 586
             |:||        | |  :|  :   :   : :||       ::  ||  | |
Db     351 ------AYYS--------PVG--KKNIYLNSGLTSTKNYGKTILTKEADLVTTHELGHNF 394

Qy     587 DNNGRKYDKNGNLDPWWSTESEEKFKEKTKCMINQYSNYYWKKAGLNVKG---------- 636
           | ::| :|                  :|  |:     :    : | |
Db     395 ---GAEHDPDG---------------LAECAPNEDQGGKYVMYPIAVSGDHENNKMFSN 435

Qy     637 --KRTLGENIADNGGLREAFR-AYRKWINDRRQGLEEPLLPGITFTNNQLFFLSYAHVRC 693
             |::: : |      :| |:    |   : |    |   ||| : ||          |
Db     436 CSKQSIYKTIESKA--QECFQERSNKVCGNSRVDEGEECDPGIMYLNND--------TCC 485

Qy     694 NSYRPEAAREQVQIGAHSPP-----QFRVNGAISNSEEFQKAFN--------------C 733
           ||       :| ||    : |     ||       :  :: |:| |              |
Db     486 NS--DCTLKEGVQCSDRNSPCCKNCQFE-----TAQKKCQEAINATCKGVSYCTGNSSEC 538

Qy     734 PP-----NSTMNRGMDSCR 747
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Db     539 PPPGNAEDDTVCLDLGKCK 557


Search completed: May 21, 2003, 18:50:38
Job time : 34 secs
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GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

Run on: May 21, 2003, 18:49:14 ; Search time 60 Seconds
(without alignments)
1238.005 Million cell updates/sec

Title: US-09-913-955A-1
Perfect score: 3958
Sequence: 1 MEAETGSSVETGKKANRGTR.....AFNCPPNSTMNRGMDSCRLW 749

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 375593 seqs, 99172665 residues

Total number of hits satisfying chosen parameters: 375593

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1332.5	33.7	779	10	US-09-905-846-2	Sequence 2, Appli
2	1223	30.9	736	9	US-09-978-295A-526	Sequence 526, App
3	1223	30.9	736	9	US-09-978-697-526	Sequence 526, App
4	1223	30.9	736	9	US-09-978-192A-526	Sequence 526, App
5	1223	30.9	736	9	US-09-999-832A-526	Sequence 526, App
6	1223	30.9	736	9	US-09-978-189-526	Sequence 526, App
7	1223	30.9	736	9	US-10-174-590-420	Sequence 420, App
8	1223	30.9	736	9	US-10-176-758-420	Sequence 420, App
9	1223	30.9	736	9	US-10-175-737-420	Sequence 420, App
10	1223	30.9	736	9	US-10-173-706-420	Sequence 420, App
11	1223	30.9	736	9	US-10-175-738-420	Sequence 420, App
12	1223	30.9	736	9	US-10-175-752-420	Sequence 420, App
13	1223	30.9	736	9	US-10-176-482-420	Sequence 420, App
14	1223	30.9	736	9	US-10-176-757-420	Sequence 420, App
15	1223	30.9	736	9	US-10-176-913-420	Sequence 420, App
16	1223	30.9	736	9	US-10-180-552-420	Sequence 420, App
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18	1223	30.9	736	9	US-10-173-700-420	Sequence 420, App
19	1223	30.9	736	9	US-10-174-572-420	Sequence 420, App
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37	1223	30.9	736	9	US-10-173-697-420	Sequence 420, App
38	1223	30.9	736	9	US-10-173-705-420	Sequence 420, App
39	1223	30.9	736	9	US-10-174-576-420	Sequence 420, App
40	1223	30.9	736	9	US-10-174-585-420	Sequence 420, App
41	1223	30.9	736	9	US-10-174-586-420	Sequence 420, App
42	1223	30.9	736	9	US-10-175-747-420	Sequence 420, App
43	1223	30.9	736	9	US-10-176-481-420	Sequence 420, App
44	1223	30.9	736	9	US-10-176-485-420	Sequence 420, App
45	1223	30.9	736	9	US-10-176-487-420	Sequence 420, App

ALIGNMENTS

RESULT 1
US-09-905-846-2
; Sequence 2, Application US/09905846
; Patent No. US20020102707A1
; GENERAL INFORMATION:
; APPLICANT: Ian Dennis Harrow
; APPLICANT: Peter Stacey
; APPLICANT: Roderick Thomas Walsh
; TITLE OF INVENTION: Compounds for the treatment of sexual dysfunction
; FILE REFERENCE: PCS10926APME
; CURRENT APPLICATION NUMBER: US/09/905,846
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 0017387.2
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/220,908
; PRIOR FILING DATE: 2000-07-26
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 779
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-905-846-2

Query Match 33.7%; Score 1332.5; DB 10; Length 779;
Best Local Similarity 39.2%; Pred. No. 3.8e-100;
Matches 284; Conservative 145; Mismatches 258; Indels 37; Gaps 17;

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Qy      42 QGLLSLQAKQEYCLKPECIEAAAAILSKVNLSVDPCDNFFRFACDGWISNNPIPEDMPSY 101
           :|:   |   | |  | |: ||| ||  :: : :|||:|::||| ||:  : |||   |
Db      77 RGIPEAQEVSEVCTTPGCVIAAARILQNMDPTTEPCDDFYQFACGGWLRRHVIPETNSRY 136

Qy     102 GVYPWLRHNVDLKLKELLEKSISRRRDTEAIQKAKILYSSCMNEKAIEKADAKPLLHILR 161
            ::  ||  ::: || :|| | :  :|  |::||: || ||||: .|||  ::||| ||
Db     137 SIFDVLRDELEVILKAVLENSTA--KDRPAVEKARTLYRSCMNQSVIEKRGSQPLLDIL- 193

Qy     162 HSPFRWPVLESNIGPEGVWSER---KFSLLQTLATFRGQYSNSVFIRLYVSPDDKASNEH 218
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Db     194 EVVGGWPVAMDR------WNETVGLEWELERQLALMNSQFNRRVLIDLFIWNDDQNSSRH 247

Qy     219 ILKLDQATLSLAVREDYLDNSTEAKSYRDALYKFMVDTAVLL--GANSSR----AEHDMK 272
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Db    248 IIYIDQPTLGMPSREYYFNGGSNRK-VREAYLQFMVSVATLLREDANLPRDSCLVQEDMV 306

Qy    273 SVLRLEIKIAEIMIPHENRTSE-AMYNKMNISELSAM--IPQFDWLGYIKKVIDTRLYPH 329
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Qy    330 LK-DISPSENVVVRVPQYFKDLFRILGSERKKTIANYLVWRMVYSRIPNLSRRFQYRWLE 388
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Db    362 VKIKLLPDEEVVVYGIPYLQNLENIIDTYSARTIQNYLVWRLVLDRIGSLSQRFKDTRVN 421

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Qy    449 MLEKENEWMDAGTKRKAKEKARAVLAKVGYPEFIMNDTH--VNEDLKAIKFSEADYFGNV 506
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Db    660 WDLADEQNVNGFNTLGENIADNGGVRQAYKAYLKWM---AEGGKDQQLPGLDLTHEQLFF 716

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Db    717 INYAQVWCGSYRPEFAIQSIKTDVHSPLKYRVLGSLQNLAAFADTFHCARGTPMH-PKER 775

Qy    746 CRLW 749
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Db    776 CRVW 779
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RESULT 2
US-09-978-295A-526
; Sequence 526, Application US/09978295A
; Patent No. US20020156006A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C11
; CURRENT APPLICATION NUMBER: US/09/978,295A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/083392
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 30.9%; Score 1223; DB 9; Length 736;
Best Local Similarity 35.2%; Pred. No. 3e-91;
Matches 267; Conservative 145; Mismatches 307; Indels 40; Gaps 18;

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Db       7 ELGAGSNVGFQKGTRQLLGSRTQLELVLAGASLLLAALLLGCLVALGVQYHRDPSHSTCL 66

Qy      56 KPECIEAAAAILSKVNLSVDPCDNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKL 115
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Db      67 TEACIRVAGKILESLDRGVSPCEDFYQFSCGGWIRRNPLPDGRSRWNTFNSLWDQNQAIL 126

Qy     116 KELLEKSISRRRDTEAIQKAKILYSSCMNEKAIEKADAKPLLHILRHSPFRWPVLESNIG 175
           | ||| : :    :|| || :  | ||:  : ||:  |:|| ::              ||
Db     127 KHLLENT-TFNSSSEAEQKTQRFYLSCLQVERIEELGAQPLRDLI----------EKIG 174

Qy     176 P---EGVWSERKFSLLQTLATFRGQYSNSVFIRLYVSPDDKASNEHILKLDQATLSLAVR 232
             | | :  |  :: |    | |  : |  :|:| | |:|| ::::::||: | |  |
Db     175 GWNITGPWDQDNF--MEVLKAVAGTYRATPFFTVYISADSKSSNSNVIQVDQSGLFLPSR 232

Qy     233 EDYLDNSTEAKSYRDALYKFMVDTAVLLGANSSRAEHDMKSVLRLEIKIAEIMIPH-ENR 291
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Db     233 DYYL-NRTANEKVLTAYLDYMEELGMLLGGRPTSTREQMQQVLELEIQLANITVPQDQRR 291

Qy     292 TSEAMYNKMNISELSAMIPQFDWLGYIKKVIDTRLYPHLKDISPSENVVVRVPQYFKDLF 351
             | :|:||:|||| |: |  ||| ::  ::          ::| || |||    .| : :
Db     292 DEEKIYHKMSISELQALAPSMDWLEFLSFLLSP------LELSDSEPVVVYGMDYLQQVS 345

Qy     352 RILGSERKKTIANYLVWRMVYSRIPNLSRRFQYRWLEFSRVIQGT-TTLLPQWDKCVNFI 410
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Db     346 ELINRTEPSILNNYLIWNLVQKTTSSLDRRFESAQEKLLETLYGTKKSCVPRWQTCISNT 405

Qy     411 ESALPYVVGKMFVDVYFQEDKKEMMEELVEGVRWAFIDMLEKENEWMDAGTKRKAKEKAR 470
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Db     406 DDALGFALGSLFVKATFDRQSKEIAEGMISEIRTAFEEAL-GQLVWMDEKTRQAAKEKAD 464

Qy     471 AVLAKVGYPEFIMNDTHVNEDLKAIKFSEADYFGNVLQTRKYLAQSDFFWLRKAVPKTEW 530
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Qy     591 RKYDKNGNLDPWWSTESEEKFKEKTKCMINQYSNYYWKKAGLNVKGKRTLGENIADNGGL 650
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RESULT 3
US-09-978-697-526
; Sequence 526, Application US/09978697
; Patent No. US20020169284A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi
;  APPLICANT:  Baker Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan
;  APPLICANT:  Ferrara, Napoleon
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, J. Christopher
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Kuo, Sophia S.
;  APPLICANT:  Napier, Mary A.
;  APPLICANT:  Pan, James;
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Shelton, David L.
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2630P1C27
;  CURRENT APPLICATION NUMBER: US/09/978,697
;  CURRENT FILING DATE:  2001-10-16
;  PRIOR APPLICATION NUMBER: 09/918585
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  Matches  267;  Conservative  145;  Mismatches  307;  Indels   40;  Gaps   18;

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RESULT 4
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; Sequence 526, Application US/09978192A
; Patent No. US20020177553A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi
;  APPLICANT:  Baker Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan
;  APPLICANT:  Ferrara, Napoleon
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, J. Christopher
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Kuo, Sophia S.
;  APPLICANT:  Napier, Mary A.
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; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C9
; CURRENT APPLICATION NUMBER: US/09/978,192A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
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Qy      56 KPECIEAAAAILSKVNLSVDPCDNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKL 115
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Db      67 TEACIRVAGKILESLDRGVSPCEDFYQFSCGGWIRRNPLPDGRSRWNTFNSLWDQNQAIL 126

Qy     116 KELLEKSISRRRDTEAIQKAKILYSSCMNEKAIEKADAKPLLHILRHSPFRWPVLESNIG 175
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Db     127 KHLLENT-TFNSSSEAEQKTQRFYLSCLQVERIEELGAQPLRDLI----------EKIG 174

Qy     176 P---EGVWSERKFSLLQTLATFRGQYSNSVFIRLYVSPDDKASNEHILKLDQATLSLAVR 232
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Db     175 GWNITGPWDQDNF--MEVLKAVAGTYRATPFFTVYISADSKSSNSNVIQVDQSGLFLPSR 232

Qy     233 EDYLDNSTEAKSYRDALYKFMVDTAVLLGANSSRAEHDMKSVLRLEIKIAEIMIPH-ENR 291
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Db     233 DYYL-NRTANEKVLTAYLDYMEELGMLLGGRPTSTREQMQQVLELEIQLANITVPQDQRR 291

Qy     292 TSEAMYNKMNISELSAMIPQFDWLGYIKKVIDTRLYPHLKDISPSENVVVRVPQYFKDLF 351
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Db     292 DEEKIYHKMSISELQALAPSMDWLEFLSFLLSP------LELSDSEPVVVYGMDYLQQVS 345

Qy     352 RILGSERKKTIANYLVWRMVYSRIPNLSRRFQYRWLEFSRVIQGT-TTLLPQWDKCVNFI 410
             ::       : |||:| :|     :| |||:    :    : ||  : :|:|  |::
Db     346 ELINRTEPSILNNYLIWNLVQKTTSSLDRRFESAQEKLLETLYGTKKSCVPRWQTCISNT 405

Qy     411 ESALPYVVGKMFVDVYFQEDKKEMMEELVEGVRWAFIDMLEKENEWMDAGTKRKAKEKAR 470
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Db     406 DDALGFALGSLFVKATFDRQSKEIAEGMISEIRTAFEEAL-GQLVWMDEKTRQAAKEKAD 464

Qy     471 AVLAKVGYPEFIMNDTHVNEDLKAIKFSEADYFGNVLQTRKYLAQSDFFWLRKAVPKTEW 530
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Db     465 AIYDMIGFPDFILEPKELDDVYDGYEISEDSFFQNMLNLYNFSAKVMADQLRKPPSRDQW 524

Qy     531 FTNPTTVNAFYSASTNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNG 590
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Qy     591 RKYDKNGNLDPWWSTESEEKFKEKTKCMINQYSNYYWKKAGLNVKGKRTLGENIADNGGL 650
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Db     584 REYDKEGNLRPWWQNESLAAFRNHTACMEEQYNQY--QVNGERLNGRQTLGENITDNGGL 641

Qy     651 REAFRAYRKWINDRRQGLEEPLLPGITFTNNQLFFLSYAHVRCNSYRPEAAREQVQIGAH 710
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Db     642 KAAYNAYKAWL--RKHG-EEQQLPAVGLTNHQLFFVGFAQVWCSVRTPESSHEGLVTDPH 698

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RESULT 5
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; Sequence 526, Application US/09999832A
; Publication No. US20020192706A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi
;  APPLICANT:  Baker Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan
;  APPLICANT:  Ferrara, Napoleon
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, J. Christopher
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Kuo, Sophia S.
;  APPLICANT:  Napier, Mary A.
;  APPLICANT:  Pan, James;
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Shelton, David L.
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2630P1C63
;  CURRENT APPLICATION NUMBER: US/09/999,832A
;  CURRENT FILING DATE:  2001-10-24
;  PRIOR APPLICATION NUMBER: 09/918585
;  PRIOR FILING DATE: 2001-07-30
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

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  Query Match             30.9%;  Score 1223;  DB 9;  Length 736;
  Best Local Similarity   35.2%;  Pred. No. 3e-91;
  Matches  267;  Conservative  145;  Mismatches  307;  Indels   40;  Gaps   18;

Qy       2 EAETGSSV--ETGKKANRGTRIAL-VVFVGGTLVLGTILF--LVSQGL-LSLQAKQEYCL 55
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Db       7 ELGAGSNVGFQKGTRQLLGSRTQLELVLAGASLLLAALLLGCLVALGVQYHRDPSHSTCL 66

Qy      56 KPECIEAAAAILSKVNLSVDPCDNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKL 115
             ||  |  ||  ::  | ||::|::|:| |||  ||:|:    :  :  |       |
Db      67 TEACIRVAGKILESLDRGVSPCEDFYQFSCGGWIRRNPLPDGRSRWNTFNSLWDQNQAIL 126

Qy     116 KELLEKSISRRRDTEAIQKAKILYSSCMNEKAIEKADAKPLLHILRHSPFRWPVLESNIG 175
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Db     127 KHLLENT-TFNSSSEAEQKTQRFYLSCLQVERIEELGAQPLRDLI----------EKIG 174

Qy     176 P---EGVWSERKFSLLQTLATFRGQYSNSVFIRLYVSPDDKASNEHILKLDQATLSLAVR 232
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Db     175 GWNITGPWDQDNF--MEVLKAVAGTYRATPFFTVYISADSKSSNSNVIQVDQSGLFLPSR 232

Qy     233 EDYLDNSTEAKSYRDALYKFMVDTAVLLGANSSRAEHDMKSVLRLEIKIAEIMIPH-ENR 291
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Db     233 DYYL-NRTANEKVLTAYLDYMEELGMLLGGRPTSTREQMQQVLELEIQLANITVPQDQRR 291

Qy     292 TSEAMYNKMNISELSAMIPQFDWLGYIKKVIDTRLYPHLKDISPSENVVVRVPQYFKDLF 351
             | :|:||:|||| |: |  ||| ::  ::          ::| || |||    | : :
Db     292 DEEKIYHKMSISELQALAPSMDWLEFLSFLLSP------LELSDSEPVVVYGMDYLQQVS 345

Qy     352 RILGSERKKTIANYLVWRMVYSRIPNLSRRFQYRWLEFSRVIQGT-TTLLPQWDKCVNFI 410
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Db     346 ELINRTEPSILNNYLIWNLVQKTTSSLDRRFESAQEKLLETLYGTKKSCVPRWQTCISNT 405

Qy     411 ESALPYVVGKMFVDVYFQEDKKEMMEELVEGVRWAFIDMLEKENEWMDAGTKRKAKEKAR 470
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Db     406 DDALGFALGSLFVKATFDRQSKEIAEGMISEIRTAFEEAL-GQLVWMDEKTRQAAKEKAD 464

Qy     471 AVLAKVGYPEFIMNDTHVNEDLKAIKFSEADYFGNVLQTRKYLAQSDFFWLRKAVPKTEW 530
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Qy     531 FTNPTTVNAFYSASTNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNG 590
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Qy     591 RKYDKNGNLDPWWSTESEEKFKEKTKCMINQYSNYYWKKAGLNVKGKRTLGENIADNGGL 650
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Db     584 REYDKEGNLRPWWQNESLAAFRNHTACMEEQYNQY--QVNGERLNGRQTLGENITDNGGL 641

Qy     651 REAFRAYRKWINDRRQGLEEPLLPGITFTNNQLFFLSYAHVRCNSYRPEAAREQVQIGAH 710
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Db     642 KAAYNAYKAWL--RKHG-EEQQLPAVGLTNHQLFFVGFAQVWCSVRTPESSHEGLVTDPH 698

Qy     711 SPPQFRVNGAISNSEEFQKAFNCPPNSTMNRGMDSCRLW 749
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Db     699 SPARFRVLGTLSNSRDFLRHFGCPVGSPMNPG-QLCEVW 736


RESULT 6
US-09-978-189-526
; Sequence 526, Application US/09978189
; Publication No. US20030004102A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi
;  APPLICANT:  Baker Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan
;  APPLICANT:  Ferrara, Napoleon
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, J. Christopher
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Kuo, Sophia S.
;  APPLICANT:  Napier, Mary A.
;  APPLICANT:  Pan, James;
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Shelton, David L.
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION:  Acids Encoding the Same
; FILE REFERENCE: P2630P1C7
; CURRENT APPLICATION NUMBER: US/09/978,189
; CURRENT FILING DATE:  2001-10-15
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; PRIOR FILING DATE: 2001-07-30
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; PRIOR APPLICATION NUMBER: 60/083742
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: 60/084366
; PRIOR FILING DATE: 1998-05-05
; PRIOR APPLICATION NUMBER: 60/084414
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084441
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084637
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084639
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084640
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084598
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-5-07
; PRIOR APPLICATION NUMBER: 60/084627
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084643
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/085339
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085338
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 30.9%; Score 1223; DB 9; Length 736;
Best Local Similarity 35.2%; Pred. No. 3e-91;
Matches 267; Conservative 145; Mismatches 307; Indels 40; Gaps 18;

```
Qy       2 EAETGSSV--ETGKKANRGTRIAL-VVFVGGTLVLGTILF--LVSQGL-LSLQAKQEYCL 55
           |   ||:|  : | :   |:|  | :|  | :|:|  :|   ||: |:          ||
Db       7 ELGAGSNVGFQKGTRQLLGSRTQLELVLAGASLLLAALLLGCLVALGVQYHRDPSHSTCL 66

Qy      56 KPECIEAAAAILSKVNLSVDPCDNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKL 115
             ||  |  ||  ::  | ||::|::|:| |||  ||:|:    :  :  |       |
Db      67 TEACIRVAGKILESLDRGVSPCEDFYQFSCGGWIRRNPLPDGRSRWNTFNSLWDQNQAIL 126

Qy     116 KELLEKSISRRRDTEAIQKAKILYSSCMNEKAIEKADAKPLLHILRHSPFRWPVLESNIG 175
           | ||| : :    :|| || :  | ||:  : ||:  |:||  ::           ||
Db     127 KHLLENT-TFNSSSEAEQKTQRFYLSCLQVERIEELGAQPLRDLI----------EKIG 174

Qy     176 P---EGVWSERKFSLLQTLATFRGQYSNSVFIRLYVSPDDKASNEHILKLDQATLSLAVR 232
           | | :  |  :: |    | |  : |  :|:| | |:|| :::::||: | |  |
Db     175 GWNITGPWDQDNF--MEVLKAVAGTYRATPFFTVYISADSKSSNSNVIQVDQSGLFLPSR 232

Qy     233 EDYLDNSTEAKSYRDALYKFMVDTAVLLGANSSRAEHDMKSVLRLEIKIAEIMIPH-ENR 291
           : || | |  :    |   :| :  :|||   :     |: || |||::| | :|  : |
Db     233 DYYL-NRTANEKVLTAYLDYMEELGMLLGGRPTSTREQMQQVLELEIQLANITVPQDQRR 291

Qy     292 TSEAMYNKMNISELSAMIPQFDWLGYIKKVIDTRLYPHLKDISPSENVVVRVPQYFKDLF 351
           | :|:||:|||| |: |  ||| ::  ::          ::| || |||    | : :
Db     292 DEEKIYHKMSISELQALAPSMDWLEFLSFLLSP------LELSDSEPVVVYGMDYLQQVS 345

Qy     352 RILGSERKKTIANYLVWRMVYSRIPNLSRRFQYRWLEFSRVIQGT-TTLLPQWDKCVNFI 410
           ::    .  : |||:| :|    :| |||:    :    : ||  : :|:|  |::
Db     346 ELINRTEPSILNNYLIWNLVQKTTSSLDRRFESAQEKLLETLYGTKKSCVPRWQTCISNT 405
```

```
Qy    411 ESALPYVVGKMFVDVYFQEDKKEMMEELVEGVRWAFIDMLEKENEWMDAGTKRKAKEKAR 470
Db    406 DDALGFALGSLFVKATFDRQSKEIAEGMISEIRTAFEEAL-GQLVWMDEKTRQAAKEKAD 464

Qy    471 AVLAKVGYPEFIMNDTHVNEDLKAIKFSEADYFGNVLQTRKYLAQSDFFWLRKAVPKTEW 530
Db    465 AIYDMIGFPDFILEPKELDDVYDGYEISEDSFFQNMLNLYNFSAKVMADQLRKPPSRDQW 524

Qy    531 FTNPTTVNAFYSASTNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNG 590
Db    525 SMTPQTVNAYYLPTKNEIVFPAGILQAPFY-ARNHPKALNFGGIGVVMGHELTHAFDDQG 583

Qy    591 RKYDKNGNLDPWWSTESEEKFKEKTKCMINQYSNYYWKKAGLNVKGKRTLGENIADNGGL 650
Db    584 REYDKEGNLRPWWQNESLAAFRNHTACMEEQYNQY--QVNGERLNGRQTLGENITDNGGL 641

Qy    651 REAFRAYRKWINDRRQGLEEPLLPGITFTNNQLFFLSYAHVRCNSYRPEAAREQVQIGAH 710
Db    642 KAAYNAYKAWL--RKHG-EEQQLPAVGLTNHQLFFVGFAQVWCSVRTPESSHEGLVTDPH 698

Qy    711 SPPQFRVNGAISNSEEFQKAFNCPPNSTMNRGMDSCRLW 749
Db    699 SPARFRVLGTLSNSRDFLRHFGCPVGSPMNPG-QLCEVW 736
```

RESULT 7
US-10-174-590-420
; Sequence 420, Application US/10174590
; Publication No. US20030008352A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Chen,Jian
; APPLICANT: Desnoyers,Luc
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Pan,James
; APPLICANT: Smith,Victoria
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C42
; CURRENT APPLICATION NUMBER: US/10/174,590
; CURRENT FILING DATE: 2002-06-18
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 420
; LENGTH: 736
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-174-590-420

Query Match 30.9%; Score 1223; DB 9; Length 736;
Best Local Similarity 35.2%; Pred. No. 3e-91;
Matches 267; Conservative 145; Mismatches 307; Indels 40; Gaps 18;

```
Qy      2 EAETGSSV--ETGKKANRGTRIAL-VVFVGGTLVLGTILF--LVSQGL-LSLQAKQEYCL 55
Db      7 ELGAGSNVGFQKGTRQLLGSRTQLELVLAGASLLLAALLLGCLVALGVQYHRDPSHSTCL 66

Qy     56 KPECIEAAAAILSKVNLSVDPCDNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKL 115
Db     67 TEACIRVAGKILESLDRGVSPCEDFYQFSCGGWIRRNPLPDGRSRWNTFNSLWDQNQAIL 126

Qy    116 KELLEKSISRRRDTEAIQKAKILYSSCMNEKAIEKADAKPLLHILRHSPFRWPVLESNIG 175
Db    127 KHLLENT-TFNSSSEAEQKTQRFYLSCLQVERIEELGAQPLRDLI----------EKIG 174

Qy    176 P---EGVWSERKFSLLQTLATFRGQYSNSVFIRLYVSPDDKASNEHILKLDQATLSLAVR 232
Db    175 GWNITGPWDQDNF--MEVLKAVAGTYRATPFFTVYISADSKSSNSNVIQVDQSGLFLPSR 232

Qy    233 EDYLDNSTEAKSYRDALYKFMVDTAVLLGANSSRAEHDMKSVLRLEIKIAEIMIPH-ENR 291
Db    233 DYYL-NRTANEKVLTAYLDYMEELGMLLGGRPTSTREQMQQVLELEIQLANITVPQDQRR 291

Qy    292 TSEAMYNKMNISELSAMIPQFDWLGYIKKVIDTRLYPHLKDISPSENVVVRVPQYFKDLF 351
Db    292 DEEKIYHKMSISELQALAPSMDWLEFLSFLLSP------LELSDSEPVVVYGMDYLQQVS 345

Qy    352 RILGSERKKTIANYLVWRMVYSRIPNLSRRFQYRWLEFSRVIQGT-TTLLPQWDKCVNFI 410
Db    346 ELINRTEPSILNNYLIWNLVQKTTSSLDRRFESAQEKLLETLYGTKKSCVPRWQTCISNT 405

Qy    411 ESALPYVVGKMFVDVYFQEDKKEMMEELVEGVRWAFIDMLEKENEWMDAGTKRKAKEKAR 470
Db    406 DDALGFALGSLFVKATFDRQSKEIAEGMISEIRTAFEEAL-GQLVWMDEKTRQAAKEKAD 464

Qy    471 AVLAKVGYPEFIMNDTHVNEDLKAIKFSEADYFGNVLQTRKYLAQSDFFWLRKAVPKTEW 530
Db    465 AIYDMIGFPDFILEPKELDDVYDGYEISEDSFFQNMLNLYNFSAKVMADQLRKPPSRDQW 524

Qy    531 FTNPTTVNAFYSASTNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNG 590
Db    525 SMTPQTVNAYYLPTKNEIVFPAGILQAPFY-ARNHPKALNFGGIGVVMGHELTHAFDDQG 583

Qy    591 RKYDKNGNLDPWWSTESEEKFKEKTKCMINQYSNYYWKKAGLNVKGKRTLGENIADNGGL 650
Db    584 REYDKEGNLRPWWQNESLAAFRNHTACMEEQYNQY--QVNGERLNGRQTLGENITDNGGL 641

Qy    651 REAFRAYRKWINDRRQGLEEPLLPGITFTNNQLFFLSYAHVRCNSYRPEAAREQVQIGAH 710
Db    642 KAAYNAYKAWL--RKHG-EEQQLPAVGLTNHQLFFVGFAQVWCSVRTPESSHEGLVTDPH 698

Qy    711 SPPQFRVNGAISNSEEFQKAFNCPPNSTMNRGMDSCRLW 749
Db    699 SPARFRVLGTLSNSRDFLRHFGCPVGSPMNPG-QLCEVW 736
```

RESULT 8
US-10-176-758-420
; Sequence 420, Application US/10176758
; Publication No. US20030008353A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Chen,Jian
; APPLICANT: Desnoyers,Luc
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Pan,James
; APPLICANT: Smith,Victoria
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C104
; CURRENT APPLICATION NUMBER: US/10/176,758
; CURRENT FILING DATE: 2002-06-21
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 420
; LENGTH: 736
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-758-420

Query Match 30.9%; Score 1223; DB 9; Length 736;
Best Local Similarity 35.2%; Pred. No. 3e-91;
Matches 267; Conservative 145; Mismatches 307; Indels 40; Gaps 18;

```
Qy      2 EAETGSSV--ETGKKANRGTRIAL-VVFVGGTLVLGTILF--LVSQGL-LSLQAKQEYCL 55
```

```
Db       7 ELGAGSNVGFQKGTRQLLGSRTQLELVLAGASLLLAALLLGCLVALGVQYHRDPSHSTCL 66

Qy      56 KPECIEAAAAILSKVNLSVDPCDNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKL 115
           ||  |  ||  ::  | ||::|::|:| |||  ||:|:    :  :  |       |
Db      67 TEACIRVAGKILESLDRGVSPCEDFYQFSCGGWIRRNPLPDGRSRWNTFNSLWDQNQAIL 126

Qy     116 KELLEKSISRRRDTEAIQKAKILYSSCMNEKAIEKADAKPLLHILRHSPFRWPVLESNIG 175
           | ||| : :    :|| || :  | ||:  : ||:  |:||  ::             ||
Db     127 KHLLENT-TFNSSSEAEQKTQRFYLSCLQVERIEELGAQPLRDLI----------EKIG 174

Qy     176 P---EGVWSERKFSLLQTLATFRGQYSNSVFIRLYVSPDDKASNEHILKLDQATLSLAVR 232
             | | :  |  :: |    | |  : |  :|:| | |:|| :::::||: | |  |
Db     175 GWNITGPWDQDNF--MEVLKAVAGTYRATPFFTVYISADSKSSNSNVIQVDQSGLFLPSR 232

Qy     233 EDYLDNSTEAKSYRDALYKFMVDTAVLLGANSSRAEHDMKSVLRLEIKIAEIMIPH-ENR 291
           : || | |  :    |  :| :  :|||   :     |: || |||::| | :|  : |
Db     233 DYYL-NRTANEKVLTAYLDYMEELGMLLGGRPTSTREQMQQVLELEIQLANITVPQDQRR 291

Qy     292 TSEAMYNKMNISELSAMIPQFDWLGYIKKVIDTRLYPHLKDISPSENVVVRVPQYFKDLF 351
             | :|:||:|||| |: |  ||| ::  ::          ::| || |||    | : :
Db     292 DEEKIYHKMSISELQALAPSMDWLEFLSFLLSP------LELSDSEPVVVYGMDYLQQVS 345

Qy     352 RILGSERKKTIANYLVWRMVYSRIPNLSRRFQYRWLEFSRVIQGT-TTLLPQWDKCVNFI 410
           ::       : |||:| :|     :| |||:    :    : ||  : :|:|  |::
Db     346 ELINRTEPSILNNYLIWNLVQKTTSSLDRRFESAQEKLLETLYGTKKSCVPRWQTCISNT 405

Qy     411 ESALPYVVGKMFVDVYFQEDKKEMMEELVEGVRWAFIDMLEKENEWMDAGTKRKAKEKAR 470
           : || : :| :||   |    ||: | ::  :| || : |  :  |||  |:: |||||
Db     406 DDALGFALGSLFVKATFDRQSKEIAEGMISEIRTAFEEAL-GQLVWMDEKTRQAAKEKAD 464

Qy     471 AVLAKVGYPEFIMNDTHVNEDLKAIKFSEADYFGNVLQTRKYLAQSDFFWLRKAVPKTEW 530
           |:   :|:|:||:    :::     : ||  :| |:|    : |:     |||   : :|
Db     465 AIYDMIGFPDFILEPKELDDVYDGYEISEDSFFQNMLNLYNFSAKVMADQLRKPPSRDQW 524

Qy     531 FTNPTTVNAFYSASTNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNG 590
             | ||||:|  : |:| |||| || ||:    :|:::|::| |||::||| || ||: |
Db     525 SMTPQTVNAYYLPTKNEIVFPAGILQAPFY-ARNHPKALNFGGIGVVMGHELTHAFDDQG 583

Qy     591 RKYDKNGNLDPWWSTESEEKFKEKTKCMINQYSNYYWKKAGLNVKGKRTLGENIADNGGL 650
           |:||| ||| |||  ||   |:  | ||  ||: |  :  |  : ||:|||||| |||||
Db     584 REYDKEGNLRPWWQNESLAAFRNHTACMEEQYNQY--QVNGERLNGRQTLGENITDNGGL 641

Qy     651 REAFRAYRKWINDRRQGLEEPLLPGITFTNNQLFFLSYAHVRCNSYRPEAAREQVQIGAH 710
           : |: ||: |:  |: | ||  || :  ||:|||| :| | |:   ||:: | :    |
Db     642 KAAYNAYKAWL--RKHG-EEQQLPAVGLTNHQLFFVGFAQVWCSVRTPESSHEGLVTDPH 698

Qy     711 SPPQFRVNGAISNSEEFQKAFNCPPNSTMNRGMDSCRLW 749
           || :||| | :||| :| : | ||  | || |   | :|
Db     699 SPARFRVLGTLSNSRDFLRHFGCPVGSPMNPG-QLCEVW 736


RESULT 9
US-10-175-737-420
; Sequence 420, Application US/10175737
; Publication No. US20030013153A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Chen,Jian
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3430R1C50
;  CURRENT APPLICATION NUMBER: US/10/175,737
;  CURRENT FILING DATE:  2002-06-19
;  Prior Application removed - See File Wrapper or Palm
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;  NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 420
;   LENGTH: 736
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-175-737-420

  Query Match             30.9%;  Score 1223;  DB 9;  Length 736;
  Best Local Similarity   35.2%;  Pred. No. 3e-91;
  Matches  267;  Conservative  145;  Mismatches  307;  Indels   40;  Gaps   18;

Qy       2 EAETGSSV--ETGKKANRGTRIAL-VVFVGGTLVLGTILF--LVSQGL-LSLQAKQEYCL 55
           |   ||:|  : | :   |:|  | :|  | :|:|  :|   ||: |:          ||
Db       7 ELGAGSNVGFQKGTRQLLGSRTQLELVLAGASLLLAALLLGCLVALGVQYHRDPSHSTCL 66

Qy      56 KPECIEAAAAILSKVNLSVDPCDNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKL 115
             ||  |  ||  ::  | ||::|::|:| |||  ||:|:    :  :  |       |
Db      67 TEACIRVAGKILESLDRGVSPCEDFYQFSCGGWIRRNPLPDGRSRWNTFNSLWDQNQAIL 126

Qy     116 KELLEKSISRRRDTEAIQKAKILYSSCMNEKAIEKADAKPLLHILRHSPFRWPVLESNIG 175
           | ||| : :    :|| || :  | ||:  : ||:  |:||  ::             ||
Db     127 KHLLENT-TFNSSSEAEQKTQRFYLSCLQVERIEELGAQPLRDLI----------EKIG 174

Qy     176 P---EGVWSERKFSLLQTLATFRGQYSNSVFIRLYVSPDDKASNEHILKLDQATLSLAVR 232
             | | :  |  :: |    | |  : |  :|:| | |:|| :::::||: | |  |
Db     175 GWNITGPWDQDNF--MEVLKAVAGTYRATPFFTVYISADSKSSNSNVIQVDQSGLFLPSR 232

Qy     233 EDYLDNSTEAKSYRDALYKFMVDTAVLLGANSSRAEHDMKSVLRLEIKIAEIMIPH-ENR 291
           : || | |  :    |  :| :  :|||   :     |: || |||::| | :|  : |
Db     233 DYYL-NRTANEKVLTAYLDYMEELGMLLGGRPTSTREQMQQVLELEIQLANITVPQDQRR 291

Qy     292 TSEAMYNKMNISELSAMIPQFDWLGYIKKVIDTRLYPHLKDISPSENVVVRVPQYFKDLF 351
             | :|:||:|||| |: |  ||| ::  ::          ::| || |||    | : :
Db     292 DEEKIYHKMSISELQALAPSMDWLEFLSFLLSP------LELSDSEPVVVYGMDYLQQVS 345

Qy     352 RILGSERKKTIANYLVWRMVYSRIPNLSRRFQYRWLEFSRVIQGT-TTLLPQWDKCVNFI 410
           ::       : |||:| :|     :| |||:    :    : ||  : :|:|  |::
Db     346 ELINRTEPSILNNYLIWNLVQKTTSSLDRRFESAQEKLLETLYGTKKSCVPRWQTCISNT 405

Qy     411 ESALPYVVGKMFVDVYFQEDKKEMMEELVEGVRWAFIDMLEKENEWMDAGTKRKAKEKAR 470
           : || : :| :||   |    ||: | ::  :| || : |  :  |||  |:: |||||
Db     406 DDALGFALGSLFVKATFDRQSKEIAEGMISEIRTAFEEAL-GQLVWMDEKTRQAAKEKAD 464

Qy     471 AVLAKVGYPEFIMNDTHVNEDLKAIKFSEADYFGNVLQTRKYLAQSDFFWLRKAVPKTEW 530
           |:   :|:|:||:    :::     : ||  :| |:|    : |:     |||   : :|
Db     465 AIYDMIGFPDFILEPKELDDVYDGYEISEDSFFQNMLNLYNFSAKVMADQLRKPPSRDQW 524

Qy     531 FTNPTTVNAFYSASTNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNG 590
             | ||||:|  : |:| |||| || ||:    :|:::|::| |||::||| || ||: |
Db     525 SMTPQTVNAYYLPTKNEIVFPAGILQAPFY-ARNHPKALNFGGIGVVMGHELTHAFDDQG 583

Qy     591 RKYDKNGNLDPWWSTESEEKFKEKTKCMINQYSNYYWKKAGLNVKGKRTLGENIADNGGL 650
           |:||| ||| |||  ||   |:  | ||  ||: |  :  |  : ||:|||||| |||||
Db     584 REYDKEGNLRPWWQNESLAAFRNHTACMEEQYNQY--QVNGERLNGRQTLGENITDNGGL 641

Qy     651 REAFRAYRKWINDRRQGLEEPLLPGITFTNNQLFFLSYAHVRCNSYRPEAAREQVQIGAH 710
           : |: ||: |:  |: | ||  || :  ||:|||| :| | |:   ||:: | :    |
Db     642 KAAYNAYKAWL--RKHG-EEQQLPAVGLTNHQLFFVGFAQVWCSVRTPESSHEGLVTDPH 698

Qy     711 SPPQFRVNGAISNSEEFQKAFNCPPNSTMNRGMDSCRLW 749
           || :||| | :||| :| : | ||  | || |   | :|
Db     699 SPARFRVLGTLSNSRDFLRHFGCPVGSPMNPG-QLCEVW 736


RESULT 10
US-10-173-706-420
; Sequence 420, Application US/10173706
; Publication No. US20030022293A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Chen,Jian
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Goddard,Audrey
```

```
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3430R1C7
;  CURRENT APPLICATION NUMBER: US/10/173,706
;  CURRENT FILING DATE:  2002-06-17
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 420
;   LENGTH: 736
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-173-706-420

  Query Match             30.9%;  Score 1223;  DB 9;  Length 736;
  Best Local Similarity   35.2%;  Pred. No. 3e-91;
  Matches  267;  Conservative  145;  Mismatches  307;  Indels   40;  Gaps   18;

Qy       2 EAETGSSV--ETGKKANRGTRIAL-VVFVGGTLVLGTILF--LVSQGL-LSLQAKQEYCL 55
Db       7 ELGAGSNVGFQKGTRQLLGSRTQLELVLAGASLLLAALLLGCLVALGVQYHRDPSHSTCL 66

Qy      56 KPECIEAAAAILSKVNLSVDPCDNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKL 115
Db      67 TEACIRVAGKILESLDRGVSPCEDFYQFSCGGWIRRNPLPDGRSRWNTFNSLWDQNQAIL 126

Qy     116 KELLEKSISRRRDTEAIQKAKILYSSCMNEKAIEKADAKPLLHILRHSPFRWPVLESNIG 175
Db     127 KHLLENT-TFNSSSEAEQKTQRFYLSCLQVERIEELGAQPLRDLI----------EKIG 174

Qy     176 P---EGVWSERKFSLLQTLATFRGQYSNSVFIRLYVSPDDKASNEHILKLDQATLSLAVR 232
Db     175 GWNITGPWDQDNF--MEVLKAVAGTYRATPFFTVYISADSKSSNSNVIQVDQSGLFLPSR 232

Qy     233 EDYLDNSTEAKSYRDALYKFMVDTAVLLGANSSRAEHDMKSVLRLEIKIAEIMIPH-ENR 291
Db     233 DYYL-NRTANEKVLTAYLDYMEELGMLLGGRPTSTREQMQQVLELEIQLANITVPQDQRR 291

Qy     292 TSEAMYNKMNISELSAMIPQFDWLGYIKKVIDTRLYPHLKDISPSENVVVRVPQYFKDLF 351
Db     292 DEEKIYHKMSISELQALAPSMDWLEFLSFLLSP------LELSDSEPVVVYGMDYLQQVS 345

Qy     352 RILGSERKKTIANYLVWRMVYSRIPNLSRRFQYRWLEFSRVIQGT-TTLLPQWDKCVNFI 410
Db     346 ELINRTEPSILNNYLIWNLVQKTTSSLDRRFESAQEKLLETLYGTKKSCVPRWQTCISNT 405

Qy     411 ESALPYVVGKMFVDVYFQEDKKEMMEELVEGVRWAFIDMLEKENEWMDAGTKRKAKEKAR 470
Db     406 DDALGFALGSLFVKATFDRQSKEIAEGMISEIRTAFEEAL-GQLVWMDEKTRQAAKEKAD 464

Qy     471 AVLAKVGYPEFIMNDTHVNEDLKAIKFSEADYFGNVLQTRKYLAQSDFFWLRKAVPKTEW 530
Db     465 AIYDMIGFPDFILEPKELDDVYDGYEISEDSFFQNMLNLYNFSAKVMADQLRKPPSRDQW 524

Qy     531 FTNPTTVNAFYSASTNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNG 590
Db     525 SMTPQTVNAYYLPTKNEIVFPAGILQAPFY-ARNHPKALNFGGIGVVMGHELTHAFDDQG 583

Qy     591 RKYDKNGNLDPWWSTESEEKFKEKTKCMINQYSNYYWKKAGLNVKGKRTLGENIADNGGL 650
Db     584 REYDKEGNLRPWWQNESLAAFRNHTACMEEQYNQY--QVNGERLNGRQTLGENITDNGGL 641

Qy     651 REAFRAYRKWINDRRQGLEEPLLPGITFTNNQLFFLSYAHVRCNSYRPEAAREQVQIGAH 710
Db     642 KAAYNAYKAWL--RKHG-EEQQLPAVGLTNHQLFFVGFAQVWCSVRTPESSHEGLVTDPH 698

Qy     711 SPPQFRVNGAISNSEEFQKAFNCPPNSTMNRGMDSCRLW 749
```

```
Db     699 SPARFRVLGTLSNSRDFLRHFGCPVGSPMNPG-QLCEVW 736

RESULT 11
US-10-175-738-420
; Sequence 420, Application US/10175738
; Publication No. US20030022294A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Chen,Jian
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3430R1C45
;  CURRENT APPLICATION NUMBER: US/10/175,738
;  CURRENT FILING DATE:  2002-06-19
;  Prior application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 420
;   LENGTH: 736
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-175-738-420

  Query Match             30.9%;  Score 1223;  DB 9;  Length 736;
  Best Local Similarity   35.2%;  Pred. No. 3e-91;
  Matches  267;  Conservative  145;  Mismatches  307;  Indels   40;  Gaps   18;

Qy       2 EAETGSSV--ETGKKANRGTRIAL-VVFVGGTLVLGTILF--LVSQGL-LSLQAKQEYCL 55
Db       7 ELGAGSNVGFQKGTRQLLGSRTQLELVLAGASLLLAALLLGCLVALGVQYHRDPSHSTCL 66

Qy      56 KPECIEAAAAILSKVNLSVDPCDNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKL 115
Db      67 TEACIRVAGKILESLDRGVSPCEDFYQFSCGGWIRRNPLPDGRSRWNTFNSLWDQNQAIL 126

Qy     116 KELLEKSISRRRDTEAIQKAKILYSSCMNEKAIEKADAKPLLHILRHSPFRWPVLESNIG 175
Db     127 KHLLENT-TFNSSSEAEQKTQRFYLSCLQVERIEELGAQPLRDLI----------EKIG 174

Qy     176 P---EGVWSERKFSLLQTLATFRGQYSNSVFIRLYVSPDDKASNEHILKLDQATLSLAVR 232
Db     175 GWNITGPWDQDNF--MEVLKAVAGTYRATPFFTVYISADSKSSNSNVIQVDQSGLFLPSR 232

Qy     233 EDYLDNSTEAKSYRDALYKFMVDTAVLLGANSSRAEHDMKSVLRLEIKIAEIMIPH-ENR 291
Db     233 DYYL-NRTANEKVLTAYLDYMEELGMLLGGRPTSTREQMQQVLELEIQLANITVPQDQRR 291

Qy     292 TSEAMYNKMNISELSAMIPQFDWLGYIKKVIDTRLYPHLKDISPSENVVVRVPQYFKDLF 351
Db     292 DEEKIYHKMSISELQALAPSMDWLEFLSFLLSP------LELSDSEPVVVYGMDYLQQVS 345

Qy     352 RILGSERKKTIANYLVWRMVYSRIPNLSRRFQYRWLEFSRVIQGT-TTLLPQWDKCVNFI 410
Db     346 ELINRTEPSILNNYLIWNLVQKTTSSLDRRFESAQEKLLETLYGTKKSCVPRWQTCISNT 405

Qy     411 ESALPYVVGKMFVDVYFQEDKKEMMEELVEGVRWAFIDMLEKENEWMDAGTKRKAKEKAR 470
Db     406 DDALGFALGSLFVKATFDRQSKEIAEGMISEIRTAFEEAL-GQLVWMDEKTRQAAKEKAD 464

Qy     471 AVLAKVGYPEFIMNDTHVNEDLKAIKFSEADYFGNVLQTRKYLAQSDFFWLRKAVPKTEW 530
Db     465 AIYDMIGFPDFILEPKELDDVYDGYEISEDSFFQNMLNLYNFSAKVMADQLRKPPSRDQW 524
```

```
Qy    531 FTNPTTVNAFYSASTNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNG 590
          | ||||:|  : |:| ||||  || ||:    :|::|::| |||::||| || ||: |
Db    525 SMTPQTVNAYYLPTKNEIVFPAGILQAPFY-ARNHPKALNFGGIGVVMGHELTHAFDDQG 583

Qy    591 RKYDKNGNLDPWWSTESEEKFKEKTKCMINQYSNYYWKKAGLNVKGKRTLGENIADNGGL 650
          |:||| ||| |||  ||   |:  | ||  ||: |  :  |  : |::|||||| |||||
Db    584 REYDKEGNLRPWWQNESLAAFRNHTACMEEQYNQY--QVNGERLNGRQTLGENITDNGGL 641

Qy    651 REAFRAYRKWINDRRQGLEEPLLPGITFTNNQLFFLSYAHVRCNSYRPEAAREQVQIGAH 710
          : |: ||: |:  |: | ||  || :  ||:|||| :| | |:   ||:: | :    |
Db    642 KAAYNAYKAWL--RKHG-EEQQLPAVGLTNHQLFFVGFAQVWCSVRTPESSHEGLVTDPH 698

Qy    711 SPPQFRVNGAISNSEEFQKAFNCPPNSTMNRGMDSCRLW 749
          || :||| | :||| :| : | ||  | || |   | :|
Db    699 SPARFRVLGTLSNSRDFLRHFGCPVGSPMNPG-QLCEVW 736


RESULT 12
US-10-175-752-420
; Sequence 420, Application US/10175752
; Publication No. US20030022295A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Chen,Jian
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3430R1C60
;  CURRENT APPLICATION NUMBER: US/10/175,752
;  CURRENT FILING DATE:  2002-06-19
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 420
;   LENGTH: 736
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-175-752-420

  Query Match             30.9%;  Score 1223;  DB 9;  Length 736;
  Best Local Similarity   35.2%;  Pred. No. 3e-91;
  Matches  267;  Conservative  145;  Mismatches  307;  Indels   40;  Gaps   18;

Qy      2 EAETGSSV--ETGKKANRGTRIAL-VVFVGGTLVLGTILF--LVSQGL-LSLQAKQEYCL 55
            |   ||:|  : | :   |:|  | :|  | :|:|  :|   ||: |:          ||
Db      7 ELGAGSNVGFQKGTRQLLGSRTQLELVLAGASLLLAALLLGCLVALGVQYHRDPSHSTCL 66

Qy     56 KPECIEAAAAILSKVNLSVDPCDNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKL 115
             ||  |  ||  ::  | ||::|::|:| |||  ||:|:    :  :  |        |
Db     67 TEACIRVAGKILESLDRGVSPCEDFYQFSCGGWIRRNPLPDGRSRWNTFNSLWDQNQAIL 126

Qy    116 KELLEKSISRRRDTEAIQKAKILYSSCMNEKAIEKADAKPLLHILRHSPFRWPVLESNIG 175
          | ||| : :    :|| || :  | ||:  : ||:  |:||  ::             ||
Db    127 KHLLENT-TFNSSSEAEQKTQRFYLSCLQVERIEELGAQPLRDLI----------EKIG 174

Qy    176 P---EGVWSERKFSLLQTLATFRGQYSNSVFIRLYVSPDDKASNEHILKLDQATLSLAVR 232
              | | :  |  :: |    | |  : |  :|:| | |:|| ::::::||: | |  |
Db    175 GWNITGPWDQDNF--MEVLKAVAGTYRATPFFTVYISADSKSSNSNVIQVDQSGLFLPSR 232

Qy    233 EDYLDNSTEAKSYRDALYKFMVDTAVLLGANSSRAEHDMKSVLRLEIKIAEIMIPH-ENR 291
          : || | |  :    |  :| :  :|||   :     |: || |||::| | :|  : |
Db    233 DYYL-NRTANEKVLTAYLDYMEELGMLLGGRPTSTREQMQQVLELEIQLANITVPQDQRR 291

Qy    292 TSEAMYNKMNISELSAMIPQFDWLGYIKKVIDTRLYPHLKDISPSENVVVRVPQYFKDLF 351
          | :|:||:|||| |: |  ||| ::  ::         ::| || |||    | : :
Db    292 DEEKIYHKMSISELQALAPSMDWLEFLSFLLSP------LELSDSEPVVVYGMDYLQQVS 345
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```
Qy    352 RILGSERKKTIANYLVWRMVYSRIPNLSRRFQYRWLEFSRVIQGT-TTLLPQWDKCVNFI 410
          ::       : |||:| :|     :| |||:    :   : ||  : :|:|  |::
Db    346 ELINRTEPSILNNYLIWNLVQKTTSSLDRRFESAQEKLLETLYGTKKSCVPRWQTCISNT 405

Qy    411 ESALPYVVGKMFVDVYFQEDKKEMMEELVEGVRWAFIDMLEKENEWMDAGTKRKAKEKAR 470
          : || : :| :||   |    ||: | ::  :| || : |  :  |||  |:: |||||
Db    406 DDALGFALGSLFVKATFDRQSKEIAEGMISEIRTAFEEAL-GQLVWMDEKTRQAAKEKAD 464

Qy    471 AVLAKVGYPEFIMNDTHVNEDLKAIKFSEADYFGNVLQTRKYLAQSDFFWLRKAVPKTEW 530
          |:   :|:|:||:    :::     : ||  :| |:|     : |:     |||   : :|
Db    465 AIYDMIGFPDFILEPKELDDVYDGYEISEDSFFQNMLNLYNFSAKVMADQLRKPPSRDQW 524

Qy    531 FTNPTTVNAFYSASTNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNG 590
          | ||||:|  : |:| ||||  || ||:    :|::|::| |||::||| || ||: |
Db    525 SMTPQTVNAYYLPTKNEIVFPAGILQAPFY-ARNHPKALNFGGIGVVMGHELTHAFDDQG 583

Qy    591 RKYDKNGNLDPWWSTESEEKFKEKTKCMINQYSNYYWKKAGLNVKGKRTLGENIADNGGL 650
          |:||| ||| |||  ||   |:  | ||  ||: |  :  |  : |::|||||| |||||
Db    584 REYDKEGNLRPWWQNESLAAFRNHTACMEEQYNQY--QVNGERLNGRQTLGENITDNGGL 641

Qy    651 REAFRAYRKWINDRRQGLEEPLLPGITFTNNQLFFLSYAHVRCNSYRPEAAREQVQIGAH 710
          : |: ||: |:  |: | ||  || :  ||:|||| :| | |:   ||:: | :    |
Db    642 KAAYNAYKAWL--RKHG-EEQQLPAVGLTNHQLFFVGFAQVWCSVRTPESSHEGLVTDPH 698

Qy    711 SPPQFRVNGAISNSEEFQKAFNCPPNSTMNRGMDSCRLW 749
          || :||| | :||| :| : | ||  | || |   | :|
Db    699 SPARFRVLGTLSNSRDFLRHFGCPVGSPMNPG-QLCEVW 736


RESULT 13
US-10-176-482-420
; Sequence 420, Application US/10176482
; Publication No. US20030022296A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Chen,Jian
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3430R1C70
;  CURRENT APPLICATION NUMBER: US/10/176,482
;  CURRENT FILING DATE:  2002-06-20
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 420
;   LENGTH: 736
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-176-482-420

  Query Match             30.9%;  Score 1223;  DB 9;  Length 736;
  Best Local Similarity   35.2%;  Pred. No. 3e-91;
  Matches  267;  Conservative  145;  Mismatches  307;  Indels   40;  Gaps   18;

Qy      2 EAETGSSV--ETGKKANRGTRIAL-VVFVGGTLVLGTILF--LVSQGL-LSLQAKQEYCL 55
            |   ||:|  : | :   |:|  | :|  | :|:|  :|   ||: |:          ||
Db      7 ELGAGSNVGFQKGTRQLLGSRTQLELVLAGASLLLAALLLGCLVALGVQYHRDPSHSTCL 66

Qy     56 KPECIEAAAAILSKVNLSVDPCDNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKL 115
             ||  |  ||  ::  | ||::|::|:| |||  ||:|:    :  :  |        |
Db     67 TEACIRVAGKILESLDRGVSPCEDFYQFSCGGWIRRNPLPDGRSRWNTFNSLWDQNQAIL 126

Qy    116 KELLEKSISRRRDTEAIQKAKILYSSCMNEKAIEKADAKPLLHILRHSPFRWPVLESNIG 175
          | ||| : :    :|| || :  | ||:  : ||:  |:||  ::             ||
```

```
Db    127 KHLLENT-TFNSSSEAEQKTQRFYLSCLQVERIEELGAQPLRDLI----------EKIG 174

Qy    176 P---EGVWSERKFSLLQTLATFRGQYSNSVFIRLYVSPDDKASNEHILKLDQATLSLAVR 232
Db    175 GWNITGPWDQDNF--MEVLKAVAGTYRATPFFTVYISADSKSSNSNVIQVDQSGLFLPSR 232

Qy    233 EDYLDNSTEAKSYRDALYKFMVDTAVLLGANSSRAEHDMKSVLRLEIKIAEIMIPH-ENR 291
Db    233 DYYL-NRTANEKVLTAYLDYMEELGMLLGGRPTSTREQMQQVLELEIQLANITVPQDQRR 291

Qy    292 TSEAMYNKMNISELSAMIPQFDWLGYIKKVIDTRLYPHLKDISPSENVVVRVPQYFKDLF 351
Db    292 DEEKIYHKMSISELQALAPSMDWLEFLSFLLSP------LELSDSEPVVVYGMDYLQQVS 345

Qy    352 RILGSERKKTIANYLVWRMVYSRIPNLSRRFQYRWLEFSRVIQGT-TTLLPQWDKCVNFI 410
Db    346 ELINRTEPSILNNYLIWNLVQKTTSSLDRRFESAQEKLLETLYGTKKSCVPRWQTCISNT 405

Qy    411 ESALPYVVGKMFVDVYFQEDKKEMMEELVEGVRWAFIDMLEKENEWMDAGTKRKAKEKAR 470
Db    406 DDALGFALGSLFVKATFDRQSKEIAEGMISEIRTAFEEAL-GQLVWMDEKTRQAAKEKAD 464

Qy    471 AVLAKVGYPEFIMNDTHVNEDLKAIKFSEADYFGNVLQTRKYLAQSDFFWLRKAVPKTEW 530
Db    465 AIYDMIGFPDFILEPKELDDVYDGYEISEDSFFQNMLNLYNFSAKVMADQLRKPPSRDQW 524

Qy    531 FTNPTTVNAFYSASTNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNG 590
Db    525 SMTPQTVNAYYLPTKNEIVFPAGILQAPFY-ARNHPKALNFGGIGVVMGHELTHAFDDQG 583

Qy    591 RKYDKNGNLDPWWSTESEEKFKEKTKCMINQYSNYYWKKAGLNVKGKRTLGENIADNGGL 650
Db    584 REYDKEGNLRPWWQNESLAAFRNHTACMEEQYNQY--QVNGERLNGRQTLGENITDNGGL 641

Qy    651 REAFRAYRKWINDRRQGLEEPLLPGITFTNNQLFFLSYAHVRCNSYRPEAAREQVQIGAH 710
Db    642 KAAYNAYKAWL--RKHG-EEQQLPAVGLTNHQLFFVGFAQVWCSVRTPESSHEGLVTDPH 698

Qy    711 SPPQFRVNGAISNSEEFQKAFNCPPNSTMNRGMDSCRLW 749
Db    699 SPARFRVLGTLSNSRDFLRHFGCPVGSPMNPG-QLCEVW 736


RESULT 14
US-10-176-757-420
; Sequence 420, Application US/10176757
; Publication No. US20030022297A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Chen,Jian
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3430R1C86
;  CURRENT APPLICATION NUMBER: US/10/176,757
;  CURRENT FILING DATE:  2002-06-20
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 420
;   LENGTH: 736
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-176-757-420

  Query Match           30.9%;  Score 1223;  DB 9;  Length 736;
  Best Local Similarity   35.2%;  Pred. No. 3e-91;
  Matches  267;  Conservative  145;  Mismatches  307;  Indels   40;  Gaps   18;

Qy      2 EAETGSSV--ETGKKANRGTRIAL-VVFVGGTLVLGTILF--LVSQGL-LSLQAKQEYCL 55
Db      7 ELGAGSNVGFQKGTRQLLGSRTQLELVLAGASLLLAALLLGCLVALGVQYHRDPSHSTCL 66

Qy     56 KPECIEAAAAILSKVNLSVDPCDNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKL 115
Db     67 TEACIRVAGKILESLDRGVSPCEDFYQFSCGGWIRRNPLPDGRSRWNTFNSLWDQNQAIL 126

Qy    116 KELLEKSISRRRDTEAIQKAKILYSSCMNEKAIEKADAKPLLHILRHSPFRWPVLESNIG 175
Db    127 KHLLENT-TFNSSSEAEQKTQRFYLSCLQVERIEELGAQPLRDLI----------EKIG 174

Qy    176 P---EGVWSERKFSLLQTLATFRGQYSNSVFIRLYVSPDDKASNEHILKLDQATLSLAVR 232
Db    175 GWNITGPWDQDNF--MEVLKAVAGTYRATPFFTVYISADSKSSNSNVIQVDQSGLFLPSR 232

Qy    233 EDYLDNSTEAKSYRDALYKFMVDTAVLLGANSSRAEHDMKSVLRLEIKIAEIMIPH-ENR 291
Db    233 DYYL-NRTANEKVLTAYLDYMEELGMLLGGRPTSTREQMQQVLELEIQLANITVPQDQRR 291

Qy    292 TSEAMYNKMNISELSAMIPQFDWLGYIKKVIDTRLYPHLKDISPSENVVVRVPQYFKDLF 351
Db    292 DEEKIYHKMSISELQALAPSMDWLEFLSFLLSP------LELSDSEPVVVYGMDYLQQVS 345

Qy    352 RILGSERKKTIANYLVWRMVYSRIPNLSRRFQYRWLEFSRVIQGT-TTLLPQWDKCVNFI 410
Db    346 ELINRTEPSILNNYLIWNLVQKTTSSLDRRFESAQEKLLETLYGTKKSCVPRWQTCISNT 405

Qy    411 ESALPYVVGKMFVDVYFQEDKKEMMEELVEGVRWAFIDMLEKENEWMDAGTKRKAKEKAR 470
Db    406 DDALGFALGSLFVKATFDRQSKEIAEGMISEIRTAFEEAL-GQLVWMDEKTRQAAKEKAD 464

Qy    471 AVLAKVGYPEFIMNDTHVNEDLKAIKFSEADYFGNVLQTRKYLAQSDFFWLRKAVPKTEW 530
Db    465 AIYDMIGFPDFILEPKELDDVYDGYEISEDSFFQNMLNLYNFSAKVMADQLRKPPSRDQW 524

Qy    531 FTNPTTVNAFYSASTNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNG 590
Db    525 SMTPQTVNAYYLPTKNEIVFPAGILQAPFY-ARNHPKALNFGGIGVVMGHELTHAFDDQG 583

Qy    591 RKYDKNGNLDPWWSTESEEKFKEKTKCMINQYSNYYWKKAGLNVKGKRTLGENIADNGGL 650
Db    584 REYDKEGNLRPWWQNESLAAFRNHTACMEEQYNQY--QVNGERLNGRQTLGENITDNGGL 641

Qy    651 REAFRAYRKWINDRRQGLEEPLLPGITFTNNQLFFLSYAHVRCNSYRPEAAREQVQIGAH 710
Db    642 KAAYNAYKAWL--RKHG-EEQQLPAVGLTNHQLFFVGFAQVWCSVRTPESSHEGLVTDPH 698

Qy    711 SPPQFRVNGAISNSEEFQKAFNCPPNSTMNRGMDSCRLW 749
Db    699 SPARFRVLGTLSNSRDFLRHFGCPVGSPMNPG-QLCEVW 736


RESULT 15
US-10-176-913-420
; Sequence 420, Application US/10176913
; Publication No. US20030022298A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Chen,Jian
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
```

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;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3430R1C66
;  CURRENT APPLICATION NUMBER: US/10/176,913
;  CURRENT FILING DATE:  2002-06-20
;  Prior Application removed - See file Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 420
;   LENGTH: 736
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-176-913-420

  Query Match             30.9%;  Score 1223;  DB 9;  Length 736;
  Best Local Similarity   35.2%;  Pred. No. 3e-91;
  Matches  267;  Conservative  145;  Mismatches  307;  Indels   40;  Gaps   18;

Qy       2 EAETGSSV--ETGKKANRGTRIAL-VVFVGGTLVLGTILF--LVSQGL-LSLQAKQEYCL 55
Db       7 ELGAGSNVGFQKGTRQLLGSRTQLELVLAGASLLLAALLLGCLVALGVQYHRDPSHSTCL 66

Qy      56 KPECIEAAAAILSKVNLSVDPCDNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKL 115
Db      67 TEACIRVAGKILESLDRGVSPCEDFYQFSCGGWIRRNPLPDGRSRWNTFNSLWDQNQAIL 126

Qy     116 KELLEKSISRRRDTEAIQKAKILYSSCMNEKAIEKADAKPLLHILRHSPFRWPVLESNIG 175
Db     127 KHLLENT-TFNSSSEAEQKTQRFYLSCLQVERIEELGAQPLRDLI----------EKIG 174

Qy     176 P---EGVWSERKFSLLQTLATFRGQYSNSVFIRLYVSPDDKASNEHILKLDQATLSLAVR 232
Db     175 GWNITGPWDQDNF--MEVLKAVAGTYRATPFFTVYISADSKSSNSNVIQVDQSGLFLPSR 232

Qy     233 EDYLDNSTEAKSYRDALYKFMVDTAVLLGANSSRAEHDMKSVLRLEIKIAEIMIPH-ENR 291
Db     233 DYYL-NRTANEKVLTAYLDYMEELGMLLGGRPTSTREQMQQVLELEIQLANITVPQDQRR 291

Qy     292 TSEAMYNKMNISELSAMIPQFDWLGYIKKVIDTRLYPHLKDISPSENVVVRVPQYFKDLF 351
Db     292 DEEKIYHKMSISELQALAPSMDWLEFLSFLLSP------LELSDSEPVVVYGMDYLQQVS 345

Qy     352 RILGSERKKTIANYLVWRMVYSRIPNLSRRFQYRWLEFSRVIQGT-TTLLPQWDKCVNFI 410
Db     346 ELINRTEPSILNNYLIWNLVQKTTSSLDRRFESAQEKLLETLYGTKKSCVPRWQTCISNT 405

Qy     411 ESALPYVVGKMFVDVYFQEDKKEMMEELVEGVRWAFIDMLEKENEWMDAGTKRKAKEKAR 470
Db     406 DDALGFALGSLFVKATFDRQSKEIAEGMISEIRTAFEEAL-GQLVWMDEKTRQAAKEKAD 464

Qy     471 AVLAKVGYPEFIMNDTHVNEDLKAIKFSEADYFGNVLQTRKYLAQSDFFWLRKAVPKTEW 530
Db     465 AIYDMIGFPDFILEPKELDDVYDGYEISEDSFFQNMLNLYNFSAKVMADQLRKPPSRDQW 524

Qy     531 FTNPTTVNAFYSASTNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNG 590
Db     525 SMTPQTVNAYYLPTKNEIVFPAGILQAPFY-ARNHPKALNFGGIGVVMGHELTHAFDDQG 583

Qy     591 RKYDKNGNLDPWWSTESEEKFKEKTKCMINQYSNYYWKKAGLNVKGKRTLGENIADNGGL 650
Db     584 REYDKEGNLRPWWQNESLAAFRNHTACMEEQYNQY--QVNGERLNGRQTLGENITDNGGL 641

Qy     651 REAFRAYRKWINDRRQGLEEPLLPGITFTNNQLFFLSYAHVRCNSYRPEAAREQVQIGAH 710
Db     642 KAAYNAYKAWL--RKHG-EEQQLPAVGLTNHQLFFVGFAQVWCSVRTPESSHEGLVTDPH 698

Qy     711 SPPQFRVNGAISNSEEFQKAFNCPPNSTMNRGMDSCRLW 749
Db     699 SPARFRVLGTLSNSRDFLRHFGCPVGSPMNPG-QLCEVW 736


Search completed: May 21, 2003, 18:55:13
Job time : 64 secs
```

GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

Run on: May 21, 2003, 18:45:44 ; Search time 48 Seconds
(without alignments)
1500.098 Million cell updates/sec

Title: US-09-913-955A-1
Perfect score: 3958
Sequence: 1 MEAETGSSVETGKKANRGTR.....AFNCPPNSTMNRGMDSCRLW 749

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1351	34.1	774	2	JC7265	neprilysin (EC 3.4
2	1283.5	32.4	750	1	HYHUN	neprilysin (EC 3.4
3	1263.5	31.9	750	1	HYRTN	neprilysin (EC 3.4
4	1260	31.8	751	1	HYRBN	neprilysin (EC 3.4
5	1257	31.8	758	2	JC2521	endothelin convert
6	1257	31.8	770	2	JC4136	endothelin convert
7	1248.5	31.5	758	2	A54667	endothelin convert
8	1243.5	31.4	754	2	A53679	endothelin convert
9	1241.5	31.4	754	2	S47268	endothelin-convert
10	1184	29.9	825	2	I46078	endothelin convert
11	1119.5	28.3	750	2	D88082	protein T05A8.4 [i
12	1014.5	25.6	766	2	T20003	hypothetical prote
13	997	25.2	590	2	C88099	protein F18A12.8 [
14	949	24.0	769	2	T24949	hypothetical prote
15	814.5	20.6	706	2	F87683	peptidase M13 fami
16	778	19.7	754	2	T16182	hypothetical prote
17	672	17.0	663	2	C70838	probable zinc meta
18	668	16.9	700	2	B82788	metallopeptidase X
19	646.5	16.3	667	2	C87236	probable zinc meta
20	606	15.3	1589	2	T22668	hypothetical prote
21	599.5	15.1	732	1	HYHUK	Kell blood group p
22	567	14.3	798	2	T28906	hypothetical prote
23	547.5	13.8	801	2	T31991	hypothetical prote
24	512.5	12.9	726	2	B88099	protein F18A12.1 [
25	511.5	12.9	823	2	T28132	hypothetical prote
26	502	12.7	627	2	F53290	endopeptidase PepO
27	495	12.5	627	2	C86850	neutral endopeptid
28	494	12.5	627	2	A47098	lactococcal endope
29	442	11.2	774	2	T31512	hypothetical prote
30	420	10.6	649	2	E88098	protein F18A12.6 [
31	417	10.5	630	2	B98058	endopeptidase O (E
32	417	10.5	630	2	F95191	endopeptidase O [i
33	410.5	10.4	534	2	T32020	hypothetical prote
34	379	9.6	684	2	T32024	hypothetical prote
35	365	9.2	564	2	T11548	probable zinc meta
36	350	8.8	651	2	T31513	hypothetical prote
37	335.5	8.5	658	2	T16040	hypothetical prote
38	325.5	8.2	732	2	T32023	hypothetical prote
39	297.5	7.5	817	2	T25758	hypothetical prote
40	297	7.5	570	2	G88098	protein F18A12.3 [
41	291	7.4	734	2	F88098	protein F18A12.4 [
42	195.5	4.9	433	2	T28805	hypothetical prote
43	185.5	4.7	550	2	D88099	protein F18A12.5 [
44	157.5	4.0	198	2	D88098	protein T06D4.5 [i
45	157.5	4.0	198	2	T32025	hypothetical prote

ALIGNMENTS

RESULT 1
JC7265
neprilysin (EC 3.4.24.11) II - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 02-Sep-2000
C;Accession: JC7265
R;Tanja, O.; Facchinetti, P.; Rose, C.; Bonhomme, M.C.; Gros, C.; Schwartz, J.C.
Biochem. Biophys. Res. Commun. 271, 565-570, 2000
A;Title: Neprilysin II: A putative novel metalloprotease and its isoforms in CNS and
A;Reference number: JC7265
A;Contents: Brain and testis
A;Accession: JC7265
A;Molecule type: mRNA
A;Residues: 1-774 <TAN>
C;Genetics:
A;Gene: nepII
C;Superfamily: neprilysin
C;Keywords: brain; glycoprotein; hydrolase; metalloproteinase; neuropeptide; testis;

Query Match 34.1%; Score 1351; DB 2; Length 774;
Best Local Similarity 38.2%; Pred. No. 1.4e-83;
Matches 289; Conservative 156; Mismatches 266; Indels 46; Gaps 18;

```
Qy      18 GTRIALVVF--VGGTL-VLGTILF-------LVSQGLLSLQAKQEYCLKPECIEAAAAIL 67
           |  : | ||  :|  | :| ::|        :| : |     | : |  | |: ||| ||
Db      39 GAIVTLGVFYSIGKQLPLLNSLLHVSRHERTVVKRVLRDSSQKSDICTTPSCVIAAARIL 98

Qy      68 SKVNLSVDPCDNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLEKSISRRR 127
           :: |  |||||:::|| ||: :: |||    | |:  ||  ::: || :|| |  : |
Db      99 QNMDQSKKPCDNFYQYACGGWLRHHVIPETNSRYSVFDILRDELEVILKGVLEDSSVQHR 158

Qy     128 DTEAIQKAKILYSSCMNEKAIEKADAKPLLHILRHSPFRWPVLESNIGPEGVWSER---K 184
           |::||| || ||||:  ||| |::|||::|      |||          |:|    |
Db     159 --PAVEKAKTLYRSCMNQSVIEKRDSEPLLNVL-DMIGGWPVAMDK------WNETMGPK 209

Qy     185 FSLLQTLATFRGQYSNSVFIRLYVSPDDKASNEHILKLDQATLSLAVREDYLDNSTEAKS 244
           : | : ||    |::  | | |::  ||: |: |:: :|| || :  || |     ::
Db     210 WELERQLAVLNSQFNRRVLIDLFIWNDDQNSSRHVIYIDQPTLGMPSREYYF--KEDSHR 267

Qy     245 YRDALYKFMVDTAVL------LGANSSRAEHDMKSVLRLEIKIAEIMIPHENRTS-EAMY 297
           |:|  :||   | :      |   :   : :|  || ||  :|   :| | |    |:|
Db     268 VREAYLQFMTSVATMLRRDLNLPGETDLVQEEMAQVLHLETHLANATVPQEKRHDVTALY 327

Qy     298 NKMNISELSAM--IPQFDWLGYIKKVIDTRLYPHLKDISPSENVVVRVPQYFKDLFRILG 355
           ::| : ||     :  |:|  :|: |: :       :: |:| |||    | ::|  |:
Db     328 HRMGLEELQERFGLKGFNWTLFIQNVLSSVQV----ELLPNEEVVVYGIPYLENLEEIID 383

Qy     356 SERKKTIANYLVWRMVYSRIPNLSRRFQYRWLEFSRVIQGTTTLLPQWDKCVNFIESALP 415
           :|: ||||||:|  || :||:||:   ::: : : |||    :| :||::: | :
Db     384 VFPAQTLQNYLVWRLVLDRIGSLSQRFKEARVDYRKALYGTTMEEVRWRECVSYVNSNME 443

Qy     416 YVVGKMFVDVYFQEDKKEMMEELVEGVRWAFIDMLEKENEWMDAGTKRKAKEKARAVLAK 475
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```
Db    444 SAVGSLYIKRAFSKDSKSIVSELIEKIRSVFVDNLDELN-WMDEESKKKAQEKALNIREQ 502

Qy    476 VGYPEFIM--NDTHVNEDLKAIKFSEADYFGNVLQTRKYLAQSDFFWLRKAVPKTEWFTN 533
Db    503 IGYPDYILEDNNRHLDEEYSSLTFSEDLYFENGLQNLKNNAQRSLKKLREKVDQNLWIIG 562

Qy    534 PTTVNAFYSASTNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNGRKY 593
Db    563 AAVVNAFYSPNRNLIVFPAGILQPPFF-SKDQPQALNFGGIGMVIGHEITHGFDDNGRNF 621

Qy    594 DKNGNLDPWWSTESEEKFKEKTKCMINQYSNYYWKKA-GLNVKGKRTLGENIADNGGLRE 652
Db    622 DKNGNMLDWWSNFSARHFRQQSQCMIYQYSNFSWELADNQNVNGFSTLGENIADNGGVRQ 681

Qy    653 AFRAYRKWINDRRQGLEEPLLPGITFTNNQLFFLSYAHVRCNSYRPEAAREQVQIGAHSP 712
Db    682 AYKAYLQWL---AEGGRDQRLPGLNLTYAQLFFINYAQVWCGSYRPEFAIQSIKTDVHSP 738

Qy    713 PQFRVNGAISNSEEFQKAFNCPPNSTMNRGMDSCRLW 749
Db    739 LKYRVLGSLQNLPGFSEAFHCPRGSPMH-PMNRCRIW 774
```

```
RESULT 2
HYHUN
neprilysin (EC 3.4.24.11) [validated] - human
N;Alternate names: CD10; common acute lymphocytic leukemia antigen; endopeptidase 24.11;
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 08-Dec-2000
C;Accession: A41387; A36173; S05275; JL0084; S00350; S02228
R;D'Adamio, L.; Shipp, M.A.; Masteller, E.L.; Reinherz, E.L.
Proc. Natl. Acad. Sci. U.S.A. 86, 7103-7107, 1989
A;Title: Organization of the gene encoding common acute lymphoblastic leukemia antigen (
A;Reference number: A41387; MUID:89386688; PMID:2528730
A;Accession: A41387
A;Molecule type: DNA
A;Residues: 1-750 <DAA>
A;Cross-references: GB:M26605
A;Note: the authors translated the codon AAC for residues 14 and 72 as Asp
R;Shipp, M.A.; Richardson, N.E.; Sayre, P.H.; Brown, N.R.; Masteller, E.L.; Clayton, L.K
Proc. Natl. Acad. Sci. U.S.A. 85, 4819-4823, 1988
A;Title: Molecular cloning of the common acute lymphoblastic leukemia antigen (CALLA) id
A;Reference number: A36173; MUID:88263038; PMID:2968607
A;Accession: A36173
A;Molecule type: mRNA
A;Residues: 1-750 <SHI>
A;Cross-references: GB:J03779
A;Note: part of this sequence was confirmed by protein sequencing
R;Jongeneel, C.V.
submitted to the EMBL Data Library, August 1988
A;Reference number: S05275
A;Accession: S05275
A;Molecule type: mRNA
A;Residues: 1-750 <JON>
A;Cross-references: EMBL:Y00811; NID:g29625; PIDN:CAA68752.1; PID:g29626
R;Letarte, M.; Vera, S.; Tran, R.; Addis, J.B.L.; Onizuka, R.J.; Quackenbush, E.J.; Jong
J. Exp. Med. 168, 1247-1253, 1988
A;Title: Common acute lymphocytic leukemia antigen is identical to neutral endopeptidase
A;Reference number: JL0084; MUID:89010526; PMID:2971756
A;Accession: JL0084
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 2-191;211-737 <LET>
A;Cross-references: EMBL:Y00811
A;Note: part of this sequence, including the amino end of the mature protein, was confir
R;Malfroy, B.; Kuang, W.J.; Seeburg, P.H.; Mason, A.J.; Schofield, P.R.
FEBS Lett. 229, 206-210, 1988
A;Title: Molecular cloning and amino acid sequence of human enkephalinase (neutral endop
A;Reference number: S00350; MUID:88152222; PMID:3162217
A;Accession: S00350
A;Molecule type: mRNA
A;Residues: 3-750 <MAL>
A;Cross-references: EMBL:X07166
A;Note: 467-Thr was also found
C;Comment: This enzyme inactivates a variety of peptide hormones, cleaving on the ami
ney.
C;Comment: This antigen is an important cell surface marker glycoprotein in the diagn
C;Genetics:
A;Gene: GDB:MME
A;Cross-references: GDB:120190; OMIM:120520
A;Map position: 3q25.1-3q25.2
A;Introns: 54/1; 66/1; 120/1; 147/1; 179/1; 218/3; 240/3; 285/3; 319/3; 365/2; 396/3;
C;Superfamily: neprilysin
C;Keywords: glycoprotein; hydrolase; metalloproteinase; oligopeptidase; surface antig
F;2-750/Product: neprilysin #status experimental <MAT>
F;16-23/Region: stop-transfer sequence
F;29-51/Domain: transmembrane #status predicted <TMN>
F;52-750/Domain: extracellular #status predicted <EXT>
F;145,285,311,325,335,628/Binding site: carbohydrate (Asn) (covalent) #status predict
F;584,588/Binding site: zinc (His) #status predicted
F;585/Active site: Glu #status predicted

  Query Match             32.4%;  Score 1283.5;  DB 1;  Length 750;
  Best Local Similarity   35.9%;  Pred. No. 5.2e-79;
  Matches  272;  Conservative  155;  Mismatches  285;  Indels   45;  Gaps   19;

Qy     13 KKANRGTRIALVVFVGGTLVLGTILFLVSQGLLSLQAKQE--YCLKPECIEAAAAILSKV 70
Db     19 KKKQRWTPLEISLSV---LVL--LLTIIAVTMIALYATYDDGICKSSDCIKSAARLIQNM 73

Qy     71 NLSVDPCDNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLEKSISRRRDTE 130
Db     74 DATTEPCTDFFKYACGGWLKRNVIPETSSRYGNFDILRDELEVVLKDVLQE--PKTEDIV 131

Qy    131 AIQKAKILYSSCMNEKAIEKADAKPLLHILRHSPFRWPVLESNIGPEGVWSER---KFSL 187
Db    132 AVQKAKALYRSCINESAIDSRGGEPLLKLL-PDIYGWPVATEN------WEQKYGASWTA 184

Qy    188 LQTLATFRGQYSNSVFIRLYVSPDDKASNEHILKLDQATLSLAVREDYLDNSTEAKSYRD 247
Db    185 EKAIAQLNSKYGKKVLINLFVGTDDKNSVNHVIHIDQPRLGLPSR-DYYECTGIYKEACT 243

Qy    248 ALYKFMVDTAVL------LGANSSRAEHDMKSVLRLEIKIAEIMIPHENRTSE-AMYNKM 300
Db    244 AYVDFMISVARLIRQEERLPIDENQLALEMNKVMELEKEIANATAKPEDRNDPMLLYNKM 303

Qy    301 NISELSAMI------PQFDWLGYIKKVIDTRLYPHLKDISPSENVVVRVPQYFKDLFRIL 354
Db    304 TLAQIQNNFSLEINGKPFSWLNFTNEIMSTVNI----SITNEEDVVVYAPEYLTKLKPIL 359

Qy    355 GSERKKTIANYLVWRMVYSRIPNLSRRFQYRWLEFSRVIQGTTTLLPQWDKCVNFIESAL 414
Db    360 TKYSARDLQNLMSWRFIMDLVSSLSRTYKESRNAFRKALYGTTSETATWRRCANYVNGNM 419

Qy    415 PYVVGKMFVDVYFQEDKKEMMEELVEGVRWAFIDMLEKENEWMDAGTKRKAKEKARAVLA 474
Db    420 ENAVGRLYVEAAFAGESKHVVEDLIAQIREVFIQTLD-DLTWMDAETKKRAEEKALAIKE 478

Qy    475 KVGYP-EFIMNDTHVNEDLKAIKFSEADYFGNVLQTRKYLAQSDFFWLRKAVPKTEWFTN 533
Db    479 RIGYPDDIVSNDNKLNNEYLELNYKEDEYFENIIQNLKFSQSKQLKKLREKVDKDEWISG 538

Qy    534 PTTVNAFYSASTNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNGRKY 593
Db    539 AAVVNAFYSSGRNQIVFPAGILQPPFF-SAQQSNSLNYGGIGMVIGHEITHGFDDNGRNF 597

Qy    594 DKNGNLDPWWSTESEEKFKEKTKCMINQYSNYYWKKA-GLNVKGKRTLGENIADNGGLRE 652
Db    598 NKDGDLVDWWTQQSASNFKEQSQCMVYQYGNFSWDLAGGQHLNGINTLGENIADNGGLGQ 657

Qy    653 AFRAYRKWINDRRQGLEEPLLPGITFTNNQLFFLSYAHVRCNSYRPEAAREQVQIGAHSP 712
Db    658 AYRAYQNYI--KKNG-EEKLLPGLDLNHKQLFFLNFAQVWCGTYRPEYAVNSIKTDVHSP 714

Qy    713 PQFRVNGAISNSEEFQKAFNCPPNSTMNRGMDSCRLW 749
```

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          ||: | : || || :||:|  || ||     ||:|
Db    715 GNFRIIGTLQNSAEFSEAFHCRKNSYMN-PEKKCRVW 750


RESULT 3
HYRTN
neprilysin (EC 3.4.24.11) - rat
N;Alternate names: CD10; common acute lymphocytic leukemia antigen; endopeptidase 24.11;
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 18-Jun-1999
C;Accession: A29295; A33521
R;Malfroy, B.; Schofield, P.R.; Kuang, W.J.; Seeburg, P.H.; Mason, A.J.; Henzel, W.J.
Biochem. Biophys. Res. Commun. 144, 59-66, 1987
A;Title: Molecular cloning and amino acid sequence of rat enkephalinase.
A;Reference number: A29295; MUID:87213218; PMID:3555489
A;Accession: A29295
A;Molecule type: mRNA
A;Residues: 1-750 <MAL>
A;Cross-references: GB:M15944; NID:g204031; PIDN:AAA41116.1; PID:g204032
A;Note: part of this sequence, including the amino end of the mature protein, was confir
R;Bateman Jr., R.C.; Jackson, D.; Slaughter, C.A.; Unnithan, S.; Chai, Y.G.; Moomaw, C.;
J. Biol. Chem. 264, 6151-6157, 1989
A;Title: Identification of the active-site arginine in rat neutral endopeptidase 24.11 (
A;Reference number: A33521; MUID:89197908; PMID:2703483
A;Accession: A33521
A;Molecule type: protein
A;Residues: 95-102,'X',104-129 <BAT>
C;Comment: This enzyme inactivates a variety of peptide hormones, cleaving on the amino
ney.
C;Superfamily: neprilysin
C;Keywords: glycoprotein; hydrolase; metalloproteinase; oligopeptidase; surface antigen;
F;9-750/Product: neprilysin #status experimental <MAT>
F;16-23/Region: stop-transfer sequence
F;29-51/Domain: transmembrane #status predicted <TMN>
F;52-750/Domain: extracellular #status predicted <EXT>
F;145,285,325,628/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;311/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;584,588/Binding site: zinc (His) #status predicted
F;585/Active site: Glu #status predicted

  Query Match             31.9%;  Score 1263.5;  DB 1;  Length 750;
  Best Local Similarity   35.7%;  Pred. No. 1.2e-77;
  Matches  270;  Conservative  151;  Mismatches  291;  Indels   45;  Gaps   19;

Qy      13 KKANRGTRIALVVFVGGTLVLGTILFLVSQGLLSLQAKQE--YCLKPECIEAAAAILSKV 70
           ||  | | : : : |   |||  :| :::  :::| | :   |   :||::|| ::  :
Db      19 KKKQRWTPLEISLSV---LVL--LLTIIAVTMIALYATYDDGICKSSDCIKSAARLIQNM 73

Qy      71 NLSVDPCDNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLEKSISRRRDTE 130
           : | :|| :||::|| ||:  | |||    |  :  ||  ::: ||::|::   :  |
Db      74 DASAEPCTDFFKYACGGWLKRNVIPETSSRYSNFDILRDELEVILKDVLQE--PKTEDIV 131

Qy     131 AIQKAKILYSSCMNEKAIEKADAKPLLHILRHSPFRWPVLESNIGPEGVWSE---RKFSL 187
           |:|||| || ||:|| ||:    :||| :|    : |||   |      | :     ::
Db     132 AVQKAKTLYRSCINESAIDSRGGQPLLTLL-PDIYGWPVASQN------WEQTYGTSWTA 184

Qy     188 LQTLATFRGQYSNSVFIRLYVSPDDKASNEHILKLDQATLSLAVREDYLDNSTEAKSYRD 247
           :::|    :|   | | :|  ||| | :||:  ||  | | |  | || : :  |
Db     185 EKSIAQLNSKYGKKVLINFFVGTDDKNSTQHIIHFDQPRLGLPSR-DYYECTGIYKEACT 243

Qy     248 ALYKFMVDTAVL------LGANSSRAEHDMKSVLRLEIKIAEIMIPHENRTSE-AMYNKM 300
           |   ||:  | |      | : ::   :|  |: || :||      |:|     :||||
Db     244 AYVDFMISVARLIRQEQRLPIDENQLSLEMNKVMELEKEIANATTKPEDRNDPMLLYNKM 303

Qy     301 NISELSAMI------PQFDWLGYIKKVIDTRLYPHLKDISPSENVVVRVPQYFKDLFRIL 354
           :::|            | |  :  ::: |      :|.  | |||  |:|   |  ||
Db     304 TLAKLQNNFSLEINGKPFSWSNFTNEIMSTVNI----NIQNEEEVVVYAPEYLTKLKPIL 359

Qy     355 GSERKKTIANYLVWRMVYSRIPNLSRRFQYRWLEFSRVIQGTTTLLPQWDKCVNFIESAL 414
           : : | : || :  : :|||::      | : : |||:    | :| |::   :
Db     360 TKYSPRDLQNLMSWRFIMDLVSSLSRNYKESRNAFRKALYGTTSETATWRRCANYVNGNM 419

Qy     415 PYVVGKMFVDVYFQEDKKEMMEELVEGVRWAFIDMLEKENEWMDAGTKRKAKEKARAVLA 474
           ||:::|:  |  : | ::|:|:  :|  ||  |: :  |||| ||:||:||| |:
Db     420 ENAVGRLYVEAAFAGESKHVVEDLIAQIREVFIQTLD-DLTWMDAETKKKAEEKALAIKE 478

Qy     475 KVGYP-EFIMNDTHVNEDLKAIKFSEADYFGNVLQTRKYLAQSDFFWLRKAVPKTEWFTN 533
           ::||| : | |:  :| :   : : | :|| |::|  |:        ||: | | || :
Db     479 RIGYPDDIISNENKLNNEYLELNYKEEEYFENIIQNLKFSQSKQLKKLREKVDKDEWISG 538

Qy     534 PTTVNAFYSASTNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNGRKY 593
           ||||||:  ||| |||| || |||       ||:|| ||:::||| |||||:||| :
Db     539 AAVVNAFYSSGRNQIVFPAGILQPPFF-SARQSNSLNYGGIGMVIGHEITHGFDDNGRNF 597

Qy     594 DKNGNLDPWWSTESEEKFKEKTKCMINQYSNYYWKKA-GLNVKGKRTLGENIADNGGLRE 652
           :|:|:|  ||: :|   ||::::||: || |: |  | | :: |  ||||||||||: :
Db     598 NKDGDLVDWWTQQSANNFKDQSQCMVYQYGNFTWDLAGGQHLNGINTLGENIADNGGIGQ 657

Qy     653 AFRAYRKWINDRRQGLEEPLLPGITFTNNQLFFLSYAHVRCNSYRPEAAREQVQIGAHSP 712
           |:|||: ::  :: | || ||||:   : ||||::| | | :|||| |   ::   |||
Db     658 AYRAYQNYV--KKNG-EEKLLPGLDLNHKQLFFLNFAQVWCGTYRPEYAVNSIKTDVHSP 714

Qy     713 PQFRVNGAISNSEEFQKAFNCPPNSTMNRGMDSCRLW 749
             ||: | : || |:|  ||:|  || ||     ||:|
Db     715 GNFRIIGTLQNSAEFADAFHCRKNSYMNPER-KCRVW 750


RESULT 4
HYRBN
neprilysin (EC 3.4.24.11) - rabbit
N;Alternate names: CD10; common acute lymphocytic leukemia antigen; endopeptidase 24.
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 18-Jun-1999
C;Accession: A29451; I46872
R;Devault, A.; Lazure, C.; Nault, C.; Le Moual, H.; Seidah, N.G.; Chretien, M.; Kahn,
EMBO J. 6, 1317-1322, 1987
A;Title: Amino acid sequence of rabbit kidney neutral endopeptidase 24.11 (enkephalin
A;Reference number: A29451; MUID:87275825; PMID:2440677
A;Accession: A29451
A;Molecule type: mRNA
A;Residues: 1-751 <DEV>
A;Cross-references: EMBL:X05338
A;Note: part of this sequence, including the amino end of the mature protein, was con
R;Kahn, P.H.; Powell, J.F.; Beaumont, A.; Roques, B.P.; Mallet, J.J.
Biochem. Biophys. Res. Commun. 145, 488-493, 1987
A;Title: An antibody purified with a lambda GT11 fusion protein precipitates enkephal
A;Reference number: I46872; MUID:87241544; PMID:3297057
A;Accession: I46872
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 207-275 <KAH>
A;Cross-references: GB:M16593; NID:g165556; PIDN:AAA53694.1; PID:g165557
C;Comment: This enzyme inactivates a variety of peptide hormones, cleaving on the ami
ney.
C;Superfamily: neprilysin
C;Keywords: glycoprotein; hydrolase; metalloproteinase; oligopeptidase; surface antig
F;2-751/Product: neprilysin #status experimental <MAT>
F;16-23/Region: stop-transfer sequence
F;29-51/Domain: transmembrane #status predicted <TMN>
F;52-751/Domain: extracellular #status predicted <EXT>
F;145,286,312,326/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;585,589/Binding site: zinc (His) #status predicted
F;586/Active site: Glu #status predicted
F;629/Binding site: carbohydrate (Asn) (covalent) #status experimental

  Query Match             31.8%;  Score 1260;  DB 1;  Length 751;
  Best Local Similarity   36.0%;  Pred. No. 2e-77;
  Matches  273;  Conservative  149;  Mismatches  290;  Indels   46;  Gaps   20;

Qy      13 KKANRGTRIALVVFVGGTLVLGTILFLVSQGLLSLQAKQE--YCLKPECIEAAAAILSKV 70
           ||  | | : : : |   |||  :| :::  :::| | :   |   :||::|| ::  :
Db      19 KKKQRWTPLEISLSV---LVL--LLTVIAVTMIALYATYDDGICKSSDCIKSAARLIQNM 73

Qy      71 NLSVDPCDNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLEKSISRRRDTE 130
           : : :|| :||::|| ||:  | |||    |  :  ||  ::: ||::|::   :  |
Db      74 DATAEPCTDFFKYACGGWLKRNVIPETSSRYSNFDILRDELEVILKDVLQE--PKTEDIV 131
```

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Qy    131 AIQKAKILYSSCMNEKAIEKADAKPLLHILRHSPFRWPVLESNIGPEGVWSE---RKFSL 187
          |:|||| || ||:|| ||:    :||| :|    : |||   |       | :     :|
Db    132 AVQKAKTLYRSCVNETAIDSRGGQPLLKLL-PDVYGWPVATQN------WEQTYGTSWSA 184

Qy    188 LQTLATFRGQYSNSVFIRLY-VSPDDKASNEHILKLDQATLSLAVREDYLDNSTEAKSYR 246
           :::|     |  | |  : |  ||| |  ||: :||  | |  | || : :   |
Db    185 EKSIAQLNSNYGKKVLINFFVVGTDDKNSMNHIIHIDQPRLGLPSR-DYYECTGIYKEAC 243

Qy    247 DALYKFMVDTAVL------LGANSSRAEHDMKSVLRLEIKIAEIMIPHENRTSE-AMYNK 299
            |   ||:  | |       |  : ::   :|  |: ||.:||      |:|     :|||
Db    244 TAYVDFMIAVAKLIRQEEGLPIDENQISVEMNKVMELEKEIANATTKSEDRNDPMLLYNK 303

Qy    300 MNISELSAMI------PQFDWLGYIKKVIDTRLYPHLKDISPSENVVVRVPQYFKDLFRI 353
          | ::::            | |  :  ::: |       :|   |:|||  |:|   |  |
Db    304 MTLAQIQNNFSLEINGKPFSWSNFTNEIMSTVNI----NIPNEEDVVVYAPEYLIKLKPI 359

Qy    354 LGSERKKTIANYLVWRMVYSRIPNLSRRFQYRWLEFSRVIQGTTTLLPQWDKCVNFIESA 413
          |     :   |   || :   : :||| ::      | : : |||:     | :| |::
Db    360 LTKYFPRDFQNLFSWRFIMDLVSSLSRTYKDSRNAFRKALYGTTSESATWRRCANYVNGN 419

Qy    414 LPYVVGKMFVDVYFQEDKKEMMEELVEGVRWAFIDMLEKENEWMDAGTKRKAKEKARAVL 473
          :   ||:::|:  |  : | ::|:|:  :|  ||  |: :  |||| ||:||:||| |:
Db    420 MENAVGRLYVEAAFAGESKHVVEDLIAQIREVFIQTLD-DLTWMDAETKKKAEEKALAIK 478

Qy    474 AKVGYP-EFIMNDTHVNEDLKAIKFSEADYFGNVLQTRKYLAQSDFFWLRKAVPKTEWFT 532
           ::||| : : ||  :| :   : : | :|| |::|  |:        ||: | | || |
Db    479 ERIGYPDDIVSNDNKLNNEYLELNYKEDEYFENIIQNLKFSQSKQLKKLREKVDKDEWIT 538

Qy    533 NPTTVNAFYSASTNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNGRK 592
              ||||||:  ||| |||| || |||   :   ||:|| ||:::||| |||||:|||
Db    539 GAAIVNAFYSSGRNQIVFPAGILQPPFF-SAQQSNSLNYGGIGMVIGHEITHGFDDNGRN 597

Qy    593 YDKNGNLDPWWSTESEEKFKEKTKCMINQYSNYYWKKA-GLNVKGKRTLGENIADNGGLR 651
          ::|:|:|  ||: :|   |||:::||: || |: |  | | :: |  ||||||||||:
Db    598 FNKDGDLVDWWTQQSANNFKEQSQCMVYQYGNFSWDLAGGQHLNGINTLGENIADNGGIG 657

Qy    652 EAFRAYRKWINDRRQGLEEPLLPGITFTNNQLFFLSYAHVRCNSYRPEAAREQVQIGAHS 711
          :|:|||: ::  :: | || |||||   : |||||::| | | :|||| |   ::   ||
Db    658 QAYRAYQNYV--KKNG-EEKLLPGIDLNHKQLFFLNFAQVWCGTYRPEYAVNSIKTDVHS 714

Qy    712 PPQFRVNGAISNSEEFQKAFNCPPNSTMNRGMDSCRLW 749
          |  ||: |:: || || :|| || || ||     ||:|
Db    715 PGNFRIIGSLQNSVEFSEAFQCPKNSYMN-PEKKCRVW 751
```

RESULT 5
JC2521
endothelin converting enzyme (EC 3.4.24.-) 1, umbilical vein endothelial cell form - hum
C;Species: Homo sapiens (man)
C;Date: 17-May-1995 #sequence_revision 14-Jul-1995 #text_change 20-Jun-2000
C;Accession: JC2521
R;Shimada, K.; Matsushita, Y.; Wakabayashi, K.; Takahashi, M.; Matsubara, A.; Iijima, Y.
Biochem. Biophys. Res. Commun. 207, 807-812, 1995
A;Title: Cloning and functional expression of human endothelin-converting enzyme cDNA.
A;Reference number: JC2521; MUID:95169128; PMID:7864876
A;Accession: JC2521
A;Molecule type: mRNA
A;Residues: 1-758 <SHI>
A;Cross-references: GB:D43698; NID:g1197803; PIDN:BAA07800.1; PID:g1197804
A;Experimental source: umbilical vein endothelial cells
C;Genetics:
A;Gene: GDB:ECE1; ECE
A;Cross-references: GDB:698357; OMIM:600423
A;Map position: 1p36.1-1p36.1
C;Superfamily: neprilysin
C;Keywords: alternative splicing; glycoprotein; hydrolase; metalloproteinase; transmembr
F;57-77/Domain: transmembrane #status predicted <TMM>
F;154,175,198,258,304,350,371,527,620,639/Binding site: carbohydrate (Asn) (covalent) #s
F;595,599/Binding site: zinc, catalytic (His) #status predicted
F;596/Active site: Glu #status predicted

Query Match 31.8%; Score 1257; DB 2; Length 758;
Best Local Similarity 37.6%; Pred. No. 3.3e-77;
Matches 281; Conservative 126; Mismatches 276; Indels 64; Gaps 21;

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Qy     21 IALVVFVGGTLVLGTILFLVSQGLLSLQAKQEYCLKPECIEAAAAILSKVNLSVDPCDNF 80
          : |||     |  | :  | : |:          ||   |:   ::||| :: :|||| :|
Db     58 VVLVVL----LAAGLVACLAALGIQYQTRSPSVCLSEACVSVTSSILSSMDPTVDPCHDF 113

Qy     81 FRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLEKSISRRRDTEAIQKAKILYS 140
          | :|| |||  ||:|:    :| :  |  :    :| ||| | :    :|| :||:: |
Db    114 FSYACGGWIKANPVPDGHSRWGTFSNLWEHNQAIIKHLLENSTA--SVSEAERKAQVYYR 171

Qy    141 SCMNEKAIEKADAKPLLHILRHSPFRWPVLESNIGPEGVWSERKFSLLQTLATFRGQYSN 200
          :|||| ||:  ||||: ::      | :        | |::  |    ||       |
Db    172 ACMNETRIEELRAKPLMELIERLG-GWNI-------TGPWAKDNFQ--DTLQVVTAHYRT 221

Qy    201 SVFIRLYVSPDDKASNEHILKLDQATLSLAVREDYLDNSTEAKSYRDALYKFMVDTAVLL 260
          | |  :||| | | || :::::||: | |  |: || | || :        :||    ||
Db    222 SPFFSVYVSADSKNSNSNVIQVDQSGLGLPSRDYYL-NKTENEKVLTGYLNYMVQLGKLL 280

Qy    261 GANSSRA-EHDMKSVLRLEIKIAEIMIPHENRTSEAM-YNKMNISELSAMIPQFDWLGYI 318
          |     |    |: :|  |  :| | || | |  | : |:|:  :||  : |  :|| :
Db    281 GGGDEEAIRPQMQQILDFETALANITIPQEKRRDEELIYHKVTAAELQTLAPAINWLPF- 339

Qy    319 KKVIDTRLYPHLKDISPSENVVVRVPQYFKDLFRILGSERKKTIANYLVWRMVYSRIPNL 378
             ::|  ||   :|: || :||   :| : :  :: :  :  : ||::| :|      |
Db    340 ---LNTIFYP--VEINESEPIVVYDKEYLEQISTLINTTDRCLLNNYMIWNLVRKTSSFL 394

Qy    379 SRRFQYRWLEFSRVIQGT-TTLLPQWDKCVNFIESALPYVVGKMFVDVYFQEDKKEMMEE 437
          :|||    :|  |: ||  | ||:|  ||:  |: | : :| |||    | || | :  |
Db    395 DQRFQDADEKFMEVMYGTKKTCLPRWKFCVSDTENNLGFALGPMFVKATFAEDSKSIATE 454

Qy    438 LVEGVRWAFIDMLEKENEWMDAGTKRKAKEKARAVLAKVGYPEFIM---------NDTHV 488
          ::  :: || : |    :|||  |:: ||||| |:   :||| |||          ||
Db    455 IILEIKKAFEESL-STLKWMDEETRKSAKEKADAIYNMIGYPNFIMDPKELDKVFNDYTA 513

Qy    489 NEDLKAIKFSEADYFGNVLQTRKYLAQSDFFW------LRKAVPKTEWFTNPTTVNAFYS 542
            ||          || | ::       :| |      ||||  : :|    |  |||:||
Db    514 VPDL---------YFENAMRF------FNFSWRVTADQLRKAPNRDQWSMTPPMVNAYYS 558

Qy    543 ASTNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNGRKYDKNGNLDPW 602
           : |:| |||| || ||:  :  |::|::| |||:|||| || ||: ||:|||:||| ||
Db    559 PTKNEIVFPAGILQAPFYTRSS-PKALNFGGIGVVVGHELTHAFDDQGREYDKDGNLRPW 617

Qy    603 WSTESEEKFKEKTKCMINQYSNYYWKKAGLNVKGKRTLGENIADNGGLREAFRAYRKWIN 662
          |   | | || :|:||: |||||     |  | |: ||||||||||||: |:|||: |:
Db    618 WKNSSVEAFKRQTECMVEQYSNY--SVNGEPVNGRHTLGENIADNGGLKAAYRAYQNWV- 674

Qy    663 DRRQGLEEPLLPGITFTNNQLFFLSYAHVRCNSYRPEAAREQVQIGAHSPPQFRVNGAIS 722
          ::  | |   || :  |||||||| :| | |:   ||:: | :    ||| :||| |::|
Db    675 -KKNGAEHS-LPTLGLTNNQLFFLGFAQVWCSVRTPESSHEGLITDPHSPSRFRVIGSLS 732

Qy    723 NSEEFQKAFNCPPNSTMNRGMDSCRLW 749
          ||:|| : | ||| | ||     | :|
Db    733 NSKEFSEHFRCPPGSPMN-PPHKCEVW 758
```

RESULT 6
JC4136
endothelin converting enzyme (EC 3.4.24.-) 1, renal adenocarcinoma form - human
C;Species: Homo sapiens (man)
C;Date: 31-Aug-1995 #sequence_revision 27-Oct-1995 #text_change 20-Jun-2000
C;Accession: JC4136; S51009; S47269
R;Yorimitsu, K.; Moroi, K.; Inagaki, N.; Saito, T.; Masuda, Y.; Masaki, T.; Seino, S.
Biochem. Biophys. Res. Commun. 208, 721-727, 1995
A;Title: Cloning and sequencing of a human endothelin converting enzyme in renal aden
A;Reference number: JC4136; MUID:95209687; PMID:7695628
A;Accession: JC4136
A;Molecule type: mRNA
A;Residues: 1-770 <YOR>
A;Cross-references: GB:D49471; NID:g695404; PIDN:BAA08442.1; PID:g695405
A;Experimental source: renal adenocarcinoma cell
A;Note: it is uncertain whether Met-1 or Met-18 is the initiator
R;Schmidt, M.; Kroeger, B.; Jacob, E.; Seulberger, H.; Subkowski, T.; Otter, R.; Meye

```
FEBS Lett. 356, 238-243, 1994
A;Title: Molecular characterization of human and bovine endothelin converting enzyme (EC
A;Reference number: S51009; MUID:95104423; PMID:7805846
A;Accession: S51009
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 18-770 <SC2>
A;Cross-references: EMBL:Z35307; NID:g535181; PIDN:CAA84548.1; PID:g535182
C;Comment: This enzyme is a phosphoramidon-sensitive, membrane-bound metalloprotease.
C;Genetics:
A;Gene: GDB:ECE1; ECE
A;Cross-references: GDB:698357; OMIM:600423
A;Map position: 1p36.1-1p36.1
C;Superfamily: neprilysin
C;Keywords: alternative splicing; glycoprotein; hydrolase; metalloproteinase; phosphopro
F;69-89/Domain: transmembrane #status predicted <TMM>
F;25/Binding site: phosphate (Thr) (covalent) #status predicted
F;166,187,210,270,316,362,383,539,632,651/Binding site: carbohydrate (Asn) (covalent) #s
F;607,611/Binding site: zinc, catalytic (His) #status predicted
F;608/Active site: Glu #status predicted

  Query Match           31.8%;  Score 1257;  DB 2;  Length 770;
  Best Local Similarity  37.6%;  Pred. No. 3.4e-77;
  Matches  281;  Conservative  126;  Mismatches  276;  Indels   64;  Gaps   21;

Qy      21 IALVVFVGGTLVLGTILFLVSQGLLSLQAKQEYCLKPECIEAAAAILSKVNLSVDPCDNF 80
           : |||      |  | : | : |:          ||    |:   ::||| :: :|||| :|
Db      70 VVLVVL----LAAGLVACLAALGIQYQTRSPSVCLSEACVSVTSSILSSMDPTVDPCHDF 125

Qy      81 FRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLEKSISRRRDTEAIQKAKILYS 140
           | :|| |||  ||:|:    :| :  |  :    :| ||| | :    :|| :||:: |
Db     126 FSYACGGWIKANPVPDGHSRWGTFSNLWEHNQAIIKHLLENSTA--SVSEAERKAQVYYR 183

Qy     141 SCMNEKAIEKADAKPLLHILRHSPFRWPVLESNIGPEGVWSERKFSLLQTLATFRGQYSN 200
           :|||  ||:  |||| :: :       | :        | |::  |    ||       |
Db     184 ACMNETRIEELRAKPLMELIERLG-GWNI-------TGPWAKDNFQ--DTLQVVTAHYRT 233

Qy     201 SVFIRLYVSPDDKASNEHILKLDQATLSLAVREDYLDNSTEAKSYRDALYKFMVDTAVLL 260
           | |  :||| | | || ::::::||: | |  |: || | || :         :||    ||
Db     234 SPFFSVYVSADSKNSNSNVIQVDQSGLGLPSRDYYL-NKTENEKVLTGYLNYMVQLGKLL 292

Qy     261 GANSSRA-EHDMKSVLRLEIKIAEIMIPHENRTSEAM-YNKMNISELSAMIPQFDWLGYI 318
           |     |    |: :|  |  :| | || | |  | : |:|:  :||  : |  :|| :
Db     293 GGGDEEAIRPQMQQILDFETALANITIPQEKRRDEELIYHKVTAAELQTLAPAINWLPF- 351

Qy     319 KKVIDTRLYPHLKDISPSENVVVRVPQYFKDLFRILGSERKKTIANYLVWRMVYSRIPNL 378
              ::|  ||   :|: || :||   :| : :  :: :  :  : ||::| :|      |
Db     352 ---LNTIFYP--VEINESEPIVVYDKEYLEQISTLINTTDRCLLNNYMIWNLVRKTSSFL 406

Qy     379 SRRFQYRWLEFSRVIQGT-TTLLPQWDKCVNFIESALPYVVGKMFVDVYFQEDKKEMMEE 437
           :|||    :|  |: ||  | ||:|  ||:  |: | : :| |||   | || | :  |
Db     407 DQRFQDADEKFMEVMYGTKKTCLPRWKFCVSDTENNLGFALGPMFVKATFAEDSKSIATE 466

Qy     438 LVEGVRWAFIDMLEKENEWMDAGTKRKAKEKARAVLAKVGYPEFIM---------NDTHV 488
           ::  :: || : |    :|||  |:: ||||| |:   :||| |||          ||
Db     467 ILILEIKKAFEESL-STLKWMDEETRKSAKEKADAIYNMIGYPNFIMDPKELDKVFNDYTA 525

Qy     489 NEDLKAIKFSEADYFGNVLQTRKYLAQSDFFW------LRKAVPKTEWFTNPTTVNAFYS 542
             ||         || | ::        :| |      |||| : :|   |  |||:|| 
Db     526 VPDL---------YFENAMRF------FNFSWRVTADQLRKAPNRDQWSMTPPMVNAYYS 570

Qy     543 ASTNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNGRKYDKNGNLDPW 602
           : |:| |||| || ||:  :  |::|::| |||:|||| || ||: ||:|||:||| ||
Db     571 PTKNEIVFPAGILQAPFYTRSS-PKALNFGGIGVVVGHELTHAFDDQGREYDKDGNLRPW 629

Qy     603 WSTESEEKFKEKTKCMINQYSNYYWKKAGLNVKGKRTLGENIADNGGLREAFRAYRKWIN 662
           |   | | || :|:||: |||||      |  | |: |||||||||||: |:||: |:
Db     630 WKNSSVEAFKRQTECMVEQYSNY--SVNGEPVNGRHTLGENIADNGGLKAAYRAYQNWV- 686

Qy     663 DRRQGLEEPLLPGITFTNNQLFFLSYAHVRCNSYRPEAAREQVQIGAHSPPQFRVNGAIS 722
           :: | |   || :  |||||||| :| | |:   ||:: | :    ||| :||| |::|
Db     687 -KKNGAEHS-LPTLGLTNNQLFFLGFAQVWCSVRTPESSHEGLITDPHSPSRFRVIGSLS 744

Qy     723 NSEEFQKAFNCPPNSTMNRGMDSCRLW 749
           ||:|| : | ||| | ||      | :|
Db     745 NSKEFSEHFRCPPGSPMN-PPHKCEVW 770


RESULT 7
A54667
endothelin converting enzyme (EC 3.4.24.-) 1 - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 05-Nov-1999
C;Accession: A54667; JC2448
R;Xu, D.; Emoto, N.; Giaid, A.; Slaughter, C.; Kaw, S.; deWit, D.; Yanagisawa, M.
Cell 78, 473-485, 1994
A;Title: ECE-1: a membrane-gound metalloprotease that catalyzes the proteolytic activ
A;Reference number: A54667; MUID:94340737; PMID:8062389
A;Accession: A54667
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-758 <XUA>
A;Cross-references: GB:U27342; NID:g897601; PIDN:AAA82928.1; PID:g897602
R;Ikura, T.; Sawamura, T.; Shiraki, T.; Hosokawa, H.; Kido, T.; Hoshikawa, H.; Shimad
Biochem. Biophys. Res. Commun. 203, 1417-1422, 1994
A;Title: cDNA cloning and expression of bovine endothelin converting enzyme.
A;Reference number: JC2448; MUID:95032010; PMID:7945289
A;Accession: JC2448
A;Molecule type: mRNA
A;Residues: 1-90,'A',92-698,'A',700-758 <IKU>
A;Cross-references: GB:S73774; NID:g688289; PIDN:AAB32062.1; PID:g688290
C;Superfamily: neprilysin
C;Keywords: hydrolase; metalloproteinase; transmembrane protein; zinc
F;57-77/Domain: transmembrane #status predicted <TMM>
F;595,599/Binding site: zinc, catalytic (His) #status predicted
F;596/Active site: Glu #status predicted

  Query Match           31.5%;  Score 1248.5;  DB 2;  Length 758;
  Best Local Similarity  37.9%;  Pred. No. 1.3e-76;
  Matches  282;  Conservative  121;  Mismatches  281;  Indels   61;  Gaps   21;

Qy      23 LVVFVGGTLVLGTILFLVSQGLLSLQAKQEYCLKPECIEAAAAILSKVNLSVDPCDNFFR 82
           ||| |   |    :  |   |:          ||   ||   ::||| :: :|||| :||
Db      57 LVVLV-ALLAAALVACLAVLGIQYQTRTPSVCLSEGCISVTSSILSSMDPTVDPCQDFFT 115

Qy      83 FACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLEKSISRRRDTEAIQKAKILYSSC 142
           :|| |||  ||:|:    :| :  |  :    :| ||| | :    :|| :||:: | :|
Db     116 YACGGWIKANPVPDGHSRWGTFSNLWEHNQAIIKHLLENSTA--SVSEAERKAQVYYRAC 173

Qy     143 MNEKAIEKADAKPLLHILRHSPFRWPVLESNIGPEGVWSERKFSLLQTLATFRGQYSNSV 202
           |||  ||:  ||||: ::       | :        | | :  |    ||       |  |
Db     174 MNETRIEELKAKPLMELIEKLG-GWNI-------TGPWDKDNFQ--DTLQVVTSHYHTSP 223

Qy     203 FIRLYVSPDDKASNEHILKLDQATLSLAVREDYLDNSTEAKSYRDALYKFMVDTAVLLGA 262
           |  :||| | | || ::::::||: | |  |: || | || :         :||    |||
Db     224 FFSVYVSADSKNSNSNVIQVDQSGLGLPSRDYYL-NKTENEKVLTGYLNYMVQLGKLLGG 282

Qy     263 NS-SRAEHDMKSVLRLEIKIAEIMIPHENRTSEAM-YNKMNISELSAMIPQFDWLGYIKK 320
           :       |: :|  |  :| | || | |  | : |:|:  :||  : |  :|| :
Db     283 GAEDTIRPQMQQILDFETALANITIPQEKRRDEELIYHKVTAAELQTLAPAINWLPF--- 339

Qy     321 VIDTRLYPHLKDISPSENVVVRVPQYFKDLFRILGSERKKTIANYLVWRMVYSRIPNLSR 380
           ::|  ||   :|: || :|:   :|   :  :: |  |  : ||::| :|      | :
Db     340 -LNTIFYP--VEINESEPIVIYDKEYLSKVSTLINSTDKCLLNNYMIWNLVRKTSSFLDQ 396

Qy     381 RFQYRWLEFSRVIQGT-TTLLPQWDKCVNFIESALPYVVGKMFVDVYFQEDKKEMMEELV 439
           |||     :|  |: ||  | ||:|  ||:  |: | : :| |||   | || | :  |::
Db     397 RFQDADEKFMEVMYGTKKTCLPRWKFCVSDTENTLGFALGPMFVKATFAEDSKNIASEII 456

Qy     440 EGVRWAFIDMLEKENEWMDAGTKRKAKEKARAVLAKVGYPEFIM---------NDTHVNE 490
             :: || : |    :|||  |:: ||||| |:   :||| |||          ||
Db     457 LEIKKAFEESL-STLKWMDEDTRKSAKEKADAIYNMIGYPNFIMDPKELDKVFNDYTAVP 515

Qy     491 DLKAIKFSEADYFGNVLQTRKYLAQSDFFW------LRKAVPKTEWFTNPTTVNAFYSAS 544
           ||         || | ::        :| |      |||| : :|   |  |||:|| :
Db     516 DL---------YFENAMRF------FNFSWRVTADQLRKAPNRDQWSMTPPMVNAYYSPT 560
```

```
Qy     545 TNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNGRKYDKNGNLDPWWS 604
           |:| |||| || ||:  :  | :|::| |||:|||| || ||: ||:|||:||| |||
Db     561 KNEIVFPAGILQAPFYTRSS-PNALNFGGIGVVVGHELTHAFDDQGREYDKDGNLRPWWK 619

Qy     605 TESEEKFKEKTKCMINQYSNYYWKKAGLNVKGKRTLGENIADNGGLREAFRAYRKWINDR 664
           | | ||::| ||: || ||      |  | |: |||||||||||: |:|||: |:  :
Db     620 NSSVEAFKQQTACMVEQYGNY--SVNGEPVNGRHTLGENIADNGGLKAAYRAYQNWV--K 675

Qy     665 RQGLEEPLLPGITFTNNQLFFLSYAHVRCNSYRPEAAREQVQIGAHSPPQFRVNGAISNS 724
           : | |:  || :  |||||||||:  | |:   ||:: | :    ||| :||| |:||||
Db     676 KNGAEQ-TLPTLGLTNNQLFFLSFGQVWCSVRTPESSHEGLITDPHSPSRFRVIGSISNS 734

Qy     725 EEFQKAFNCPPNSTMNRGMDSCRLW 749
           :|| : |:||| | ||     | :|
Db     735 KEFSEHFHCPPGSPMN-PHHKCEVW 758


RESULT 8
A53679
endothelin converting enzyme (EC 3.4.24.-) - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 20-Jun-2000
C;Accession: A53679; JU0189
R;Shimada, K.; Takahashi, M.; Tanzawa, K.
J. Biol. Chem. 269, 18275-18278, 1994
A;Title: Cloning and functional expression of endothelin-converting enzyme from rat endo
A;Reference number: A53679; MUID:94308046; PMID:8034569
A;Accession: A53679
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-754 <SHI>
A;Cross-references: GB:D29683; NID:g529084; PIDN:BAA06152.1; PID:g529085
C;Superfamily: neprilysin
C;Keywords: glycoprotein; hydrolase; metalloproteinase; transmembrane protein; zinc
F;1-52/Domain: intracellular #status predicted <INT>
F;53-73/Domain: transmembrane #status predicted <TMM>
F;74-754/Domain: extracellular #status predicted <EXT>
F;129/Binding site: substrate (Arg) #status predicted
F;150,171,194,254,300,346,367,523,616,635/Binding site: carbohydrate (Asn) (covalent) #s
F;591,595/Binding site: zinc, catalytic (His) #status predicted
F;592/Active site: Glu #status predicted

  Query Match             31.4%;  Score 1243.5;  DB 2;  Length 754;
  Best Local Similarity   37.5%;  Pred. No. 2.7e-76;
  Matches  277;  Conservative  129;  Mismatches  284;  Indels   49;  Gaps   19;

Qy      23 LVVFVGGTLVLGTILFLVSQGLLSLQAKQEYCLKPECIEAAAAILSKVNLSVDPCDNFFR 82
           ||| |   |  |  : |:         ||   |:   ::||: :: :|||| :||
Db      53 LVVLV-TLLAAGLVACLAALGIQYRTRTPPVCLTEACVSVTSSILNSMDPTVDPCQDFFS 111

Qy      83 FACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLEKSISRRRDTEAIQKAKILYSSC 142
           :|| |||  ||:|:    :| :  |  :    :| ||| | :    :|| :||:: | :|
Db     112 YACGGWIKANPVPDGHSRWGTFSNLWEHNQAIIKHLLENSTASA--SEAEKKAQVYYRAC 169

Qy     143 MNEKAIEKADAKPLLHILRHSPFRWPVLESNIGPEGVWSERKFSLLQTLATFRGQYSNSV 202
           |||  ||:  ||||: ::      | :       | |:: |    ||      |  |
Db     170 MNETRIEELRAKPLMELIEKLG-GWNI-------TGPWAKDNFQ--DTLQVVTAHYRTSP 219

Qy     203 FIRLYVSPDDKASNEHILKLDQATLSLAVREDYLDNSTEAKSYRDALYKFMVDTAVLL-G 261
           |  :||| | | || :::::||: | |  |: || | || :        :||    || |
Db     220 FFSVYVSADSKNSNSNVIQVDQSGLGLPSRDYYL-NKTENEKVLTGYLNYMVQLGKLLGG 278

Qy     262 ANSSRAEHDMKSVLRLEIKIAEIMIPHENRTSEAM-YNKMNISELSAMIPQFDWLGYIKK 320
           :       |: :|  |  :| | || | |  | : |:|:  :||  : |  :|| ::
Db     279 GDEDSIRPQMQQILDFETALANITIPQEKRRDEELIYHKVTAAELQTLAPAINWLPFLNA 338

Qy     321 VIDTRLYPHLKDISPSENVVVRVPQYFKDLFRILGSERKKTIANYLVWRMVYSRIPNLSR 380
           :     ||   :|: || :||   :| : :  :: |  |  : ||::| :|      | :
Db     339 I----FYP--VEINESEPIVVYDKEYLRQVSTLINSTDKCLLNNYMMWNLVRKTSSFLDQ 392

Qy     381 RFQYRWLEFSRVIQGT-TTLLPQWDKCVNFIESALPYVVGKMFVDVYFQEDKKEMMEELV 439
           ||| . :|  |: ||  | ||:|  ||:  |: | : :| |||   | || | :  |::
```

```
Db     393 RFQDADEKFMEVMYGTKKTCLPRWKFCVSDTENNLGFALGPMFVKATFAEDSKNIASEII 452

Qy     440 EGVRWAFIDMLEKENEWMDAGTKRKAKEKARAVLAKVGYPEFIM---------NDTHVNE 490
             :: || : |    :|||  |:| ||||| |:   :||| |||          ||
Db     453 LEIKKAFEESL-STLKWMDEDTRRSAKEKADAIYNMIGYPNFIMDPKELDKVFNDYTAVP 511

Qy     491 DLKAIKFSEADYFGNVLQTRKYLAQSDFFWLRKAVPKTEWFTNPTTVNAFYSASTNQIRF 550
           ||          || | ::   :  :     ||||  : :|   |  |||:|| : |:| |
Db     512 DL---------YFENAMRFFNFSLRVTADQLRKAPNRDQWSMTPPMVNAYYSPTKNEIVF 562

Qy     551 PAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNGRKYDKNGNLDPWWSTESEEK 610
           ||| || ||:  :  | :|::| |||:|||| || ||: ||:|||:||| |||    | |
Db     563 PAGILQAPFYTRSS-PNALNFGGIGVVVGHELTHAFDDQGREYDKDGNLRPWWKNSSVEA 621

Qy     611 FKEKTKCMINQYSNYYWKKAGLNVKGKRTLGENIADNGGLREAFRAYRKWINDRRQGLEE 670
           ||::|:||: ||:||      |  | |: ||||||||||||: |:|||: |:  :: | |:
Db     622 FKQQTECMVQQYNNY--SVNGEPVNGRHTLGENIADNGGLKAAYRAYQNWV--KKNGAEQ 677

Qy     671 PLLPGITFTNNQLFFLSYAHVRCNSYRPEAAREQVQIGAHSPPQFRVNGAISNSEEFQKA 730
            :|| :  |:|||||| :| | |:   ||:: | :    ||| :||| |::|||:|| :
Db     678 -ILPTLGLTSNQLFFLGFAQVWCSVRTPESSHEGLITDPHSPSRFRVIGSLSNSKEFSEH 736

Qy     731 FNCPPNSTMNRGMDSCRLW 749
           | ||  | ||     | :|
Db     737 FRCPLGSPMN-PRHKCEVW 754


RESULT 9
S47268
endothelin-converting enzyme (EC 3.4.24.-) 1 - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 08-Oct-1999
C;Accession: S51010; S47268
R;Schmidt, M.; Kroeger, B.; Jacob, E.; Seulberger, H.; Subkowski, T.; Otter, R.; Meye
FEBS Lett. 356, 238-243, 1994
A;Title: Molecular characterization of human and bovine endothelin converting enzyme
A;Reference number: S51009; MUID:95104423; PMID:7805846
A;Accession: S51010
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-754 <SC2>
A;Cross-references: EMBL:Z35306; NID:g535074; PIDN:CAA84547.1; PID:g535075
C;Superfamily: neprilysin
C;Keywords: hydrolase; metalloproteinase; zinc
F;591,595/Binding site: zinc, catalytic (His) #status predicted
F;592/Active site: Glu #status predicted

  Query Match             31.4%;  Score 1241.5;  DB 2;  Length 754;
  Best Local Similarity   37.9%;  Pred. No. 3.7e-76;
  Matches  282;  Conservative  120;  Mismatches  282;  Indels   61;  Gaps   21;

Qy      23 LVVFVGGTLVLGTILFLVSQGLLSLQAKQEYCLKPECIEAAAAILSKVNLSVDPCDNFFR 82
           ||| |   |    :  |   |:          ||   ||   ::||| :: :|||| :||
Db      53 LVVLV-ALLAAALVACLAVLGIQYQTRTPSVCLSEACISVTSSILSSMDPTVDPCQDFFT 111

Qy      83 FACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLEKSISRRRDTEAIQKAKILYSSC 142
           :|| |||  ||:|:    :| :  |  :    :| ||| | :    :|| :| :  | :|
Db     112 YACGGWIKANPVPDGHSRWGTFSNLWEHNQAIIKHLLENSTA--SVSEAERKDQEYYRAC 169

Qy     143 MNEKAIEKADAKPLLHILRHSPFRWPVLESNIGPEGVWSERKFSLLQTLATFRGQYSNSV 202
           |||  ||:  ||||: ::      | :       | :  |    ||      |  |
Db     170 MNETRIEELKAKPLMELIEKLG-GWNI-------TGPWDKDNFQ--DTLQVVTSHYHTSP 219

Qy     203 FIRLYVSPDDKASNEHILKLDQATLSLAVREDYLDNSTEAKSYRDALYKFMVDTAVLLGA 262
           |  :||| | | || ::::::||: | |  |: || | || :        :||    |||
Db     220 FFSVYVSADSKNSNSNVIQVDQSGLGLPSRDYYL-NKTENEKVLTGYLNYMVQLGKLLGG 278

Qy     263 NS-SRAEHDMKSVLRLEIKIAEIMIPHENRTSEAM-YNKMNISELSAMIPQFDWLGYIKK 320
            :       |: :|  |  :| | || | |  | : |:|:  :||  : |  :|| :
Db     279 GAEDTIRPQMQQILDFETALANITIPQEKRRDEELIYHKVTAAELQTLAPAINWLPF--- 335

Qy     321 VIDTRLYPHLKDISPSENVVVRVPQYFKDLFRILGSERKKTIANYLVWRMVYSRIPNLSR 380
           ::|  ||   :|: || :|:   :|   :  :: |  |  : ||::| :|      | :
```

```
Db    336 -LNTIFYP--VEINESEPIVIYDKEYLSKVSTLINSTDKCLLNNYMIWNLVRKTSSFLDQ 392

Qy    381 RFQYRWLEFSRVIQGT-TTLLPQWDKCVNFIESALPYVVGKMFVDVYFQEDKKEMMEELV 439
          |||    :|  |: ||  | ||:|  ||:  |: | : :| |||   | || | :  |::
Db    393 RFQDADEKFMEVMYGTKKTCLPRWKFCVSDTENTLGFALGPMFVKATFAEDSKNIASEII 452

Qy    440 EGVRWAFIDMLEKENEWMDAGTKRKAKEKARAVLAKVGYPEFIM---------NDTHVNE 490
            :: || : |    :|||  |:: ||||| |:   :||| |||          ||
Db    453 LEIKKAFEESL-STLKWMDEDTRKSAKEKADAIYNMIGYPNFIMDPKELDKVFNDYTAVP 511

Qy    491 DLKAIKFSEADYFGNVLQTRKYLAQSDFFW------LRKAVPKTEWFTNPTTVNAFYSAS 544
          ||         || | ::        :| |      ||||  : :|   |  |||:|| :
Db    512 DL---------YFENAMRF------FNFSWRVTADQLRKAPNRDQWSMTPPMVNAYYSPT 556

Qy    545 TNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNGRKYDKNGNLDPWWS 604
          |:| |||| || ||:  :  | :|::| |||:|||| || ||: ||:|||:||| |||
Db    557 KNEIVFPAGILQAPFYTRSS-PNALNFGGIGVVVGHELTHAFDDQGREYDKDGNLRPWWK 615

Qy    605 TESEEKFKEKTKCMINQYSNYYWKKAGLNVKGKRTLGENIADNGGLREAFRAYRKWINDR 664
            | | ||::| ||: || ||    |  | |: ||||||||||||: |:|||: |:  :
Db    616 NSSVEAFKQQTACMVEQYGNY--SVNGEPVNGRHTLGENIADNGGLKAAYRAYQNWV--K 671

Qy    665 RQGLEEPLLPGITFTNNQLFFLSYAHVRCNSYRPEAAREQVQIGAHSPPQFRVNGAISNS 724
          : | |:  || :  ||||||||:| | |:   ||:: | :    ||| :||| |:||||
Db    672 KNGAEQ-TLPTLGLTNNQLFFLSFAQVWCSVRTPESSHEGLITDPHSPSRFRVIGSISNS 730

Qy    725 EEFQKAFNCPPNSTMNRGMDSCRLW 749
          :|| : |:||| | ||     | :|
Db    731 KEFSEHFHCPPGSPMN-PHHKCEVW 754


RESULT 10
I46078
endothelin converting enzyme (EC 3.4.24.-) 2 - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 20-Sep-1999
C;Accession: I46078
R;Emoto, N.; Yanagisawa, M.
J. Biol. Chem. 270, 15262-15268, 1995
A;Title: Endothelin-converting enzyme-2 is a membrane-bound, phosphoramidon-sensitive me
A;Reference number: A57042; MUID:95318093; PMID:7797512
A;Accession: I46078
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-825 <EMO>
A;Cross-references: EMBL:U27341; NID:g897599; PID:g897600
C;Genetics:
A;Gene: ECE-2
C;Superfamily: neprilysin
C;Keywords: hydrolase; metalloproteinase

  Query Match             29.9%;  Score 1184;  DB 2;  Length 825;
  Best Local Similarity   35.1%;  Pred. No. 3.4e-72;
  Matches  265;  Conservative  138;  Mismatches  313;  Indels   38;  Gaps   18;

Qy      4 ETGSSVETGKKANRGTRIALVVFVGGTLVLGTILF--LVSQGL-LSLQAKQEYCLKPECI 60
            | |    | :     |:: ||:  | :|:|  :|   ||: |:           ||   ||
Db    102 EAGFRKRTSRLLGLHTQLELVL-AGVSLLLAALLLGCLVALGVQYHRDPSHSTCLTEACI 160

Qy     61 EAAAAILSKVNLSVDPCDNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLE 120
            |  ||  ::  | ||::|::|:| |||  ||:|:     :      |       || |||
Db    161 RVAGKILESLDRGVSPCEDFYQFSCGGWIRRNPLPDGRSRWNNSNSLWDQNQAILKHLLE 220

Qy    121 KSISRRRDTEAIQKAKILYSSCMNEKAIEKADAKPLLHILRHSPFRWPVLESNIG---PE 177
            : :    :|| :| :  | ||:  : ||:  |    | ||        |   ||
Db    221 NT-TFNSSSEAERKTQRFYLSCLQVERIEELGA----HALRD-------LIDKIGGWNVT 268

Qy    178 GVWSERKFSLLQTLATFRGQYSNSVFIRLYVSPDDKASNEHILKLDQATLSLAVREDYLD 237
          | | :  |  :: |    | |  : |  :||| | |:|| :|:::||: | |  |: ||
Db    269 GPWDQDNF--MEVLKAVAGTYRATPFFTVYVSADSKSSNSNIIQVDQSGLFLPSRDYYL- 325

Qy    238 NSTEAKSYRDALYKFMVDTAVLLGANSSRAEHDMKSVLRLEIKIAEIMIPH-ENRTSEAM 296
          | |  :    |   :| :  :|||   :     |: || |||::| | :|  : |  | :

Db    326 NRTANEKVLTAYLDYMEELGMLLGGQPTSTREQMRQVLELEIQLANITVPQDQRRDEEKI 385

Qy    297 YNKMNISELSAMIPQFDWLGYIKKVIDTRLYPHLKDISPSENVVVRVPQYFKDLFRILGS 356
          |:||:|:|| |: |  ||| ::  ::          ::  || |||     | : :  ::
Db    386 YHKMSIAELQALAPSMDWLEFLSFLLSP------LELGDSEPVVVYGTDYLQQVSELINR 439

Qy    357 ERKKTIANYLVWRMVYSRIPNLSRRFQYRWLEFSRVIQGT-TTLLPQWDKCVNFIESALP 415
              : |||:| :|      :|  ||:     :    : ||  :  |:|  |::  : ||
Db    440 TEPSVLNNYLIWNLVQKTTSSLDHRFESAQEKLLETLYGTKKSCTPRWQTCISNTDDALG 499

Qy    416 YVVGKMFVDVYFQEDKKEMMEELVEGVRWAFIDMLEKENEWMDAGTKRKAKEKARAVLAK 475
          : :| :||    |     ||: | ::  :| || : |      |||  |:: |||||  |:
Db    500 FALGSLFVKATFDRQSKEIAEGMISEIRVAFEEAL-GHLVWMDEKTRQAAKEKADAIYDM 558

Qy    476 VGYPEFIMNDTHVNEDLKAIKFSEADYFGNVLQTRKYLAQSDFFWLRKAVPKTEWFTNPT 535
          :|:|:|||:    :::     : ||  :| |:|    : |:     |||   : :|    |
Db    559 IGFPDFILEPKELDDVYDGYEVSEDSFFQNMLNLYNFSAKVMADQLRKPPSRDQWSMTPQ 618

Qy    536 TVNAFYSASTNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNGRKYDK 595
          ||||:|  : |:| |||| || ||:    :|:::|::| |||::||| || ||: ||:|||
Db    619 TVNAYYLPTKNEIVFPAGILQAPFY-TCNHPQALNFGGIGVVMGHELTHAFDDQGREYDK 677

Qy    596 NGNLDPWWSTESEEKFKEKTKCMINQYSNYYWKKAGLNVKGKRTLGENIADNGGLREAFR 655
          |||  |||  ||   |:  | |:  ||| |  :  |  : |::|||||||||||:. |:
Db    678 EGNLRPWWQNESLAAFRNHTACIEEQYSQY--QVNGEKLNGRQTLGENIADNGGLKAAYN 735

Qy    656 AYRKWINDRRQGLEEPLLPGITFTNNQLFFLSYAHVRCNSYRPEAAREQVQIGAHSPPQF 715
          ||: |:  |: | ||  || :  ||:||||: :| | |:   ||:: | :    ||| :|
Db    736 AYKAWL--RKHG-EEQQLPAVGLTNHQLFFVGFAQVWCSVRTPESSHEGLVTDPHSPARF 792

Qy    716 RVNGAISNSEEFQKAFNCPPNSTMNRGMDSCRLW 749
          || | :||| :| : | ||  | || |   | :|
Db    793 RVLGTLSNSRDFLRHFGCPVGSPMNSG-QLCEVW 825


RESULT 11
D88082
protein T05A8.4 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001
C;Accession: D88082
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating bio
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999;
A;Accession: D88082
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-750 <STO>
A;Cross-references: GB:chr_II; PIDN:AB95021.1; PID:g2746865; GSPDB:GN00020; CESP:T05A
C;Genetics:
A;Gene: T05A8.4
A;Map position: 2
C;Superfamily: neprilysin

  Query Match             28.3%;  Score 1119.5;  DB 2;  Length 750;
  Best Local Similarity   32.4%;  Pred. No. 7e-68;
  Matches  250;  Conservative  150;  Mismatches  324;  Indels   47;  Gaps   15;

Qy      2 EAETGSSVETGKKANRGTR----IALVVFVGGTLVLGTILFLVSQGLLSLQAKQEYCLKP 57
            : | |::   |   :| ||    |||:: :   ||||  ::       :: :   : || |
Db      4 DEEDGTTKSPG---SRWTRIWAIIALILLILFLLVLGAAIYF----YINYKDSSDVCLSP 56

Qy     58 ECIEAAAAILSKVNLSVDPCDNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKE 117
            ||: |: ||| :| ||||||:|: |||  ||  :|||:| ||    :  |  :::  |||
Db     57 GCIKTASVILSSMNSSVDPCDDFYEFACGQWIKGHPIPDDAPSVSNFENLGQDLEFALKE 116

Qy    118 LL-EKSISRRRDTEAIQKAKILYSSCMNEKAIEKADAKPLLHILRHSPFRWPVLESNIGP 176
          || |       :| |: |||  |: |:||  |          ::: |   || |   : |
Db    117 LLDENDEPYDYETSAVGKAKYFYNLCLNESEILDNWRTTFDEVVK-SFGGWPSLGHQMKP 175
```

```
Qy    177 EGVWSERKFSLLQTLATFRGQYSNSVFIRLYVSPDDKASNEHILKLDQATLSLAVREDYL 236
Db    176 DA-------SIEMLYADMVAKFKADSLFKATVQPDDKNSQRHVLLIDQPQLNLFARDFYV 228

Qy    237 DNSTEAKSYRDALYKFMVDTAVLLGANSSRAEHDMKSVLRLEIKIAEIMIPHENRTSEA- 295
Db    229 AAENEE---RMAYLQLIRDVLILLDADRTRATLDAKEIIDFETALANITMADEHRHDIAE 285

Qy    296 MYNKMNISELSAMIPQFDWLGYIKKVIDTRLYPHLKDISPSEN--VVVRVPQYFKDLFRI 353
Db    286 LYTKITLGEMRRSLPHFNWPLFFNRMFKDLHEKNGKRITFDDNTEVVVYGYEFLRRLDVL 345

Qy    354 LGSERKKTIANYLVWRMVY-SRIPNLSRRFQYRWLEFSRVIQGTTTLLPQWDKCVNFIES 412
Db    346 IPQYDNRLIVNYLEWCWFFKTMLRDLPDPFALTIFKFYKTLNIMNVQKVRWHGCVTRINS 405

Qy    413 ALPYVVGKMFVDVYFQEDKKEMMEELVEGVRWAFIDMLEKENEWMDAGTKRKAKEKARAV 472
Db    406 LMPMATSAIYVKNHFDHEAKQQVEEMISLIMESFVDLLLSE-DWLTKETKQTAKQKVNEM 464

Qy    473 LAKVGYPEFIMNDTHVNEDLKAIKFSEADYFGNVLQTRKYLAQSDFFWLRKAVPKTEWFT 532
Db    465 KRKIGYPDYLNDPAAVNNEYKTFKVYPGHYYQTKFSFYEQYQRDVLERITEAVDRERWVA 524

Qy    533 NPTTVNAFYSASTNQIR--------------FPAGELQKPFFWGTEYPRSLSYGAIGVIV 578
Db    525 GAALVNAFYSPNTNEISKFLGTLTQKFKFSVFPAGILQ-PVFYSKDFPSSMNFGGIGVVI 583

Qy    579 GHEFTHGFDNNGRKYDKNGNLDPWWSTESEEKFKEKTKCMINQYSNYYWKKAGLNVKGKR 638
Db    584 GHEITHGFDDRGRLYDNLGNIRQWWDNATISKFEHKAQCIEKQYSSYVLDQINMQINGKS 643

Qy    639 TLGENIADNGGLREAFRAYRKWINDRRQGLEEPLLPGITFTNNQLFFLSYAHVRCNSYRP 698
Db    644 TKGENIADNGGLKQAYRAYKKY---EKRHSRPPRLPGVNLTHDQLFFLNYAQIWCGTMND 700

Qy    699 EAAREQVQIGAHSPPQFRVNGAISNSEEFQKAFNCPPNSTMNRGMDSCRLW 749
Db    701 KEAIRKLRTSEHSPGPIRVKGPLSNSYDFAKAYNCEPGSQMN-PREKCRVW 750
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RESULT 12
T20003
hypothetical protein ZK20.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C;Accession: T20003; T27775
R;Gajadsty, S.
submitted to the EMBL Data Library, March 1996
A;Reference number: Z19209
A;Accession: T20003
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-766 <WIL>
A;Cross-references: EMBL:Z69902; PIDN:CAA93770.1; GSPDB:GN00020; CESP:ZK20.6
A;Experimental source: clone C47D12
R;Gajadsty, S.
submitted to the EMBL Data Library, March 1996
A;Reference number: Z20417
A;Accession: T27775
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-766 <WI2>
A;Cross-references: EMBL:Z69904; PIDN:CAA93782.1; GSPDB:GN00020; CESP:ZK20.6
A;Experimental source: clone ZK20
C;Genetics:
A;Gene: CESP:ZK20.6
A;Map position: 2
A;Introns: 11/1; 334/3; 439/1; 692/2; 734/2
C;Superfamily: neprilysin

Query Match 25.6%; Score 1014.5; DB 2; Length 766;
Best Local Similarity 31.8%; Pred. No. 9.6e-61;

Matches 223; Conservative 157; Mismatches 292; Indels 29; Gaps 17;

```
Qy     61 EAAAAILSKVNLSVDPCDNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLE 120
Db     83 EASRLLQKSLNLSLDPCDDFFEYACRAWVDSHPIPDDLTSYSQFTATREKVLAEMRKLYE 142

Qy    121 KSISRRRDTEAIQKAKILYSSCMNEKAIEKADAKPLLHILRHSPFRWPVLESNIGPEGVW 180
Db    143 DNTS-IPTSKSIALIKQIYNTCMDTEKHNAVGARDLLEKIKTYGY-WPMVHNE-----KW 195

Qy    181 SERKFSLLQTLATFRGQYSNSVFIRLYVSPDDKASNEHILKLDQATLSL--AVREDYLDN 238
Db    196 RESTFDLTKLLSNTIQSRDVSVFFDFGPAEDSRNVSRRLLSFDQGSLGLGYSTRDYYLDE 255

Qy    239 ---STEAKSYRD---ALYKFMVDTAVLLGANSSRAEHDMKSVLRLEIKIAEIMIPHENRT 292
Db    256 KKYEKQMKAYRKYTIGKVRYYTEDAG-MAVNESKIESDVDEIIAFEKEWAQILVAEEDRR 314

Qy    293 S-EAMYNKMNISELSAMIPQFDWLGYIKKVIDTRLYPHLKDISPSENVVVRVPQYFKDLF 351
Db    315 NYTKLYNVRRRFDDLKEYMSIIDWKKLTLSTTPFLVHSYLK-TNPS--IIISDVEYLQKMN 371

Qy    352 RILGSERKKTIANYLVWRMVYSRIPNLSRRFQYRWLEFSRVIQGTTTLLPQWDKCVNFIE 411
Db    372 TLLQNTDPRIVTNYILLRWAGSWSQEIGKKYEDLQQEFAFQMYGRKQRQPRWKDCVSSAG 431

Qy    412 SALPYVVGKMFVDVYFQEDKKEMMEELVEGVRWAFIDMLEKENEWMDAGTKRKAKEKARA 471
Db    432 GKLSYASGSMYVRKYFDANAKNTTLDMITDLQEAFRNMMH-ANDWMDAETKKYALEKADQ 490

Qy    472 VLAKVGYPEFIMNDTHVNEDLKAIKFSEADYFGNVLQTRKYLAQSDFFWLR--KAVPKTE 529
Db    491 MLKQIGYPDFILNDEKLDDWYKGLEGAPEDSFSQLVE-KSIQWRNNFYYRRLLEPVNRFE 549

Qy    530 WFTNPTTVNAFYSASTNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNN 589
Db    550 FISSAAVVNAFYSPTRNAIAFPAGILQQPFF-DARFPKALNYGGIGAVIGHEITHGFDDT 608

Qy    590 GRKYDKNGNLDPWWSTESEEKFKEKTKCMINQYSNYYWKKAGLNVKGKRTLGENIADNGG 649
Db    609 GRQFDNVGNLRDWWDNTTSSKFNERTQCIIEQYADVKLRGTDLRINGKLTQGENIADNGG 668

Qy    650 LREAFRAYRKWINDRRQGLEEPLLPGI-TFTNNQLFFLSYAHVRCNSYRPEAAREQVQIG 708
Db    669 IKQAFKAYKSYL--EKHGGQEARLPQFESLTNEQLFFVGYAQVWCGAKTPETKTLLLLTD 726

Qy    709 AHSPPQFRVNGAISNSEEFQKAFNCPPNSTMNRGMDSCRLW 749
Db    727 PHSPETARVNTVLTNQPEFAEAFKCPAGSPMN-PTKRCVVW 766
```

RESULT 13
C88099
protein F18A12.8 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C;Accession: C88099
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating bio
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999;
A;Accession: C88099
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-590 <STO>
A;Cross-references: GB:chr_II; PIDN:AB66079.1; PID:g2315629; GSPDB:GN00020; CESP:F18A
C;Genetics:
A;Gene: F18A12.8
A;Map position: 2

Query Match 25.2%; Score 997; DB 2; Length 590;

```
  Best Local Similarity   34.8%;  Pred. No. 9.9e-60;
  Matches  214;  Conservative  120;  Mismatches  237;  Indels   44;  Gaps   14;

Qy    154 KPLLHILRHSPFRWPVLESNIGPEGVWSERKFSLLQTLATFRGQYSNSVFIRLYVSPDDK 213
          :||   |      ||:|: |      | : ||:    |   |  |   || :||:  | |
Db      1 RPLFETLTELG-EWPLLQEN------WDKTKFNFTSLLVNSRRDYGVDVFFQLYIYADSK 53

Qy    214 ASNEHILKLDQATLSLA-VREDYLDNSTEAKSYRDALYKFMVDTAVLL--GANSSRAEH- 269
          :: : | :||:||:|     ||  |:|   |:  |  |::   | ||    | :|:|
Db     54 NTSRNTLFIDQSTLALGRGTRDYYLNTTLFSSHMTAYRKYLRQIAHLLKTDGNLTRSESE 113

Qy    270 ---DMKSVLRLEIKIAEIMIPH-ENRTSEAMYNKMNISELSAMIPQFDWLGYIKKVIDTR 325
             |:: ::  ||::|:|::   | | :  :|||  | :|  ::|| ||:
Db    114 MNADIEKIIDFEIELAKIIVAEDERRNNTRLYNKRQIQDLYNLLPQVDWV---------- 163

Qy    326 LYPHLKDISPSE---------NVVVRVPQYFKDLFRILGSERKKTIANYLVWRMVYSRIP 376
            | : |:||:          :::   :| : :  ::       : ||::||:| | :
Db    164 --PFFQSIAPSDLTHLFHNETEIIICEIEYLQHVSELIEKTDVGLLTNYVLWRVVQSNVR 221

Qy    377 NLSRRFQYRWLEFSRVIQGTTTLLPQWDKCVNFIESALPYVVGKMFVDVYFQEDKKEMME 436
          |  ||:    :| :|: |     |:|  |     : ||   | ::|  :|||  |
Db    222 YLDERFEDIKQDFLKVMTGQQQSPPRWKDCAQVPSTVLPLAAGAIYVQAHFQESDKHEAL 281

Qy    437 ELVEGVRWAFIDMLEKENEWMDAGTKRKAKEKARAVLAKVGYPEFIMNDTHVNEDLKAIK 496
          ::  :| :| |:: ::|:|||  ||  | ||| :::  :|||:   :   :::    :
Db    282 RMIMHLRNSFADLV-RQNDWMDEETKAVAIEKANSMINNIGYPDVTNDLPKLDKQYLGLS 340

Qy    497 FSEADYFGNVLQTRKYLAQS-DFFWLRKAVPKTEWFTNPTTVNAFYSASTNQIRFPAGEL 555
          |::| :  :::      || :|  | |   | |:  :|  ||||||   | | |||| |
Db    341 ISDSDTYYYIMKKSVVWMQSREFQKLTKPFDKHEFDISPAVVNAFYSPEKNAITFPAGIL 400

Qy    556 QKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNGRKYDKNGNLDPWWSTESEEKFKEKT 615
          | ||| || :|::::|||| ::||| |||||: | :|||:|||  |||  |   |  :
Db    401 QPPFFSGT-FPKAVNYGAIGAVIGHEITHGFDDQGSQYDKDGNLHNWWSESSLNSFDTRR 459

Qy    616 KCMINQYSNYYWKKAGLNVKGKRTLGENIADNGGLREAFRAYRKWINDRRQGLEEPLLPG 675
          :|:: || ||   |    | || | |||||||||::|||:||:|:: :     ||| |||
Db    460 RCIVEQYGNYTVPKTNFRVNGKLTQGENIADNGGVKEAFQAYQKYVTENG---EEPRLPG 516

Qy    676 I-TFTNNQLFFLSYAHVRCNSYRPEAAREQVQIGAHSPPQFRVNGAISNSEEFQKAFNCP 734
          :  :|| |:||:|||  |   :  || :||    |||  ||| | :|| : |   : ||
Db    517 LQQYTNEQIFFVSYAHFWCGKKKEAAAMQQVLTDEHSPEVFRVIGVLSNMQAFADVYKCP 576

Qy    735 PNSTMNRGMDSCRLW 749
          |: :|     | :|
Db    577 RNAPVNPD-HKCIVW 590


RESULT 14
T24949
hypothetical protein T16A9.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C;Accession: T24949
R;McMurray, A.
submitted to the EMBL Data Library, July 1996
A;Reference number: Z19959
A;Accession: T24949
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-769 <WIL>
A;Cross-references: EMBL:Z77135; PIDN:CAB00879.1; GSPDB:GN00023; CESP:T16A9.4
A;Experimental source: clone T16A9
C;Genetics:
A;Gene: CESP:T16A9.4
A;Map position: 5
A;Introns: 15/2; 59/1; 105/3; 202/1; 336/3; 371/3; 393/1; 424/2; 457/3; 571/1; 637/2; 67
C;Superfamily: neprilysin

  Query Match           24.0%;  Score 949;  DB 2;  Length 769;
  Best Local Similarity   30.6%;  Pred. No. 2.7e-56;
  Matches  224;  Conservative  147;  Mismatches  277;  Indels   84;  Gaps   22;

Qy     54 CLKPECIEAAAAILSKVNLSVDPCDNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNV-- 111
          |   ||:  |  :   :|  ::||::|: |||  :  |  :| : |       |||  :
Db     86 CTSRECVRLAGFLAENLNSKINPCEDFYEFACGNYGLNKNLPANKP-------LRHTISD 138

Qy    112 -----DLKLKELLEKSISRRRDTEAIQK-----AKILYSSCMNEKAIEKADAKPLLHILR 161
               : ::| :|:  ||      | :|     ||  |  |::|: :|    : :  | :
Db    139 VQSRLNKQVKSMLQSPIS------ANEKPWDKVAKGYYQKCLDEEELESTGVEAMRDIAK 192

Qy    162 HSPFRWPVLESNIGPEGVWS---ERKFSLLQTLATFRGQYSNSVFIRLYVSPDDKASNEH 218
             || || :   |  ||   | : :|:  |        |:| : : |: |   |:
Db    193 RIG-GWPTLEGDKWQE--WSHSWEEQIALVLNLTGV-----NAVILEMAVTHDPSNSSRS 244

Qy    219 ILKLDQATLSLAVREDYLD--NSTEAKSYRDALYKFMVDTAVLLGANSSRAEHDMKSVLR 276
          :::|||       |  ||   |    ::|       |  ||| |||: : || :|   :
Db    245 VIELDQPKWGAGSRYPYLSGANDPMLRNYT----TLMKMTAVALGADPAIAEKEMNEAME 300

Qy    277 LEIKI----AEIMIPHENRTSEAMYNKMNISELSAMIPQFDWLGYIKKVIDTRLYPHLKD 332
          |:|:    |: |:    |  |   |:  : :| :: |  ::  |:| |     :  |
Db    301 FELKLVNFSADDMV---RRDPERGNNRFELWQLKSVFPFINFEKYLKTV-----FKELVA 352

Qy    333 ISPSENVVVRVPQYFKDLFRILGSERKKTIANYLVWRMVYSRIPNLSRRFQYRWLEFSRV 392
          :||:  |:||   ||  :  :| |  |: :|||: ||:|    | |    :  : :|
Db    353 LSPNHTVIVREIDYFVGIQHVLQSTPKRVLANYISWRLVQGFSPFLPPSAREPFYQFKAN 412

Qy    393 IQGTTTLLP--QWDKCVNFIESALPYVVGKMFVDVYFQEDK-KEMMEELVEGVRWAFIDM 449
          |      |  :|: ||       :   ||::||: :|::::  : | ||   ::  ||
Db    413 QTGMFNSPPPDRWEDCVTLSVIMMDMPVGRLFVENFFEKERAMKKMTELTSYLKNEFIKQ 472

Qy    450 LEKENEWMDAGTKRKAKEKARAVLAKVGYPEFIMNDTHVNEDLKAIKFSEADYFGNVLQT 509
          |    :|||  |:|:|  ||  :  | |:|  : ||| : ::           :| :::
Db    473 LH-VLDWMDEITRRRAISKANMIEYKSGFPMVLFNDTWMEKN----------WGMIIKP 520

Qy    510 RKYLAQ----------SDFFWLRKAVPKTEWFTNPTTVNAFYSASTNQIRFPAGELQKP 558
          |:||              :  | : : :: || :|  |:|:|: : |:: |||| :| |
Db    521 REYLLHLTIRVKLVRFTEELLRLDQPLDRSMWFQSPAQVDAYYAPNNNEMIFPAGIMQFP 580

Qy    559 FFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNGRKYDKNGNLDPWWSTESEEKFKEKTKCM 618
          |      |  ::|| :| ::||| :| ||: | :||: |||: ||  |:|||| |||:|
Db    581 FL-TLGVPNYITYGMVGAVIGHEVSHAFDDQGGQYDEMGNLNDWWDAETEEKFIEKTRCF 639

Qy    619 INQYSNYYWKKAGLNVKGKRTLGENIADNGGLREAFRAYRKWINDRRQGLEEPLLPGI-T 677
          : || | :  :| ::: |: :||||||||||:: || ||: |      |: || |||
Db    640 VRQYENVHVVEADIHLNGQLSLGENIADNGGVKTAFNAYKAW-KSNTTGISEPALPGFQN 698

Qy    678 FTNNQLFFLSYAHVRCNSYRPEAAREQVQIGAHSPPQFRVNGAISNSEEFQKAFNCPPNS 737
          ||: |:|||:||:  |:  ||:   : :    |:| ::|    : |  || ||| ||  |
Db    699 FTSQQMFFLAYANNWCSLVRPKHYIQIILTDVHAPSKYRAMIPLQNRPEFAKAFQCPIGS 758

Qy    738 TMNRGMDSCRLW 749
          ||     |::|
Db    759 PMNPER-KCQVW 769


RESULT 15
F87683
peptidase M13 family protein [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
C;Accession: F87683
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg,
 B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Ko
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: F87683
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-706 <STO>
A;Cross-references: GB:AE005673; NID:g13425232; PIDN:AAK25466.1; GSPDB:GN00148
C;Genetics:
A;Gene: CC3504
C;Superfamily: neprilysin
```

Query Match 20.6%; Score 814.5; DB 2; Length 706;
Best Local Similarity 30.6%; Pred. No. 3.1e-47;
Matches 229; Conservative 109; Mismatches 316; Indels 95; Gaps 20;

```
Qy      40 VSQGLLSLQAKQEY-CLKPECI-----------EAAAAI--------------LSKVNLS 73
           :|       || ::: |:   |:           ||| :               || :: :
Db      14 LSLSAFGAQAHEKHACIDDACVMQSLLPSITAGGAAADVASLESPRFGTWGFDLSGMDTT 73

Qy      74 VDPCDNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLEKSISRRRDTEAIQ 133
           | | ::|::||   | :   || |   || :  |    : : | ::| : : :  |
Db      74 VKPGEDFYKFANGAWDARTQIPSDRTRYGNFDKLAELSEARTKAIIEAAAANKAATGDTA 133

Qy     134 KAKILYSSCMNEKAIEKADAKPLLHILRHSPFRWPVLESNIGPEGVWSERKFSLLQTLAT 193
           |    | : |:|  ||| ||||:      :|:   :             ||        |
Db     134 KVGAAYRAFMDEAGIEKLDAKPI------APYLAEI------------RKVKSKDEFTT 174

Qy     194 FRGQYSNSVF---IRLYVSPDDKASNEHILKLDQATLSLAVREDYLDNSTEAKSYRDALY 250
           |: | : |   : | :| | |    : :      |||  |: |||     |   | |
Db     175 LMGKSSTTPFTSLLGLGISTDAKNPKAYAVYAGAGGLSLPDRDYYLDAKFADKK---AAY 231

Qy     251 KFMVDTAVLLGANSSRAEHDMKSVLRLEIKIAEIMIPH-ENRTSEAMYNKMNISELSAMI 309
           |:  : :      |||  |:|:  | |:||:     | |  :  ||   ::|| ||
Db     232 LAYVEKLLTMAGWDKPAEH-AKAVVDFETKLAEVTWTRAERRDRDKTYNPATLAELQAMS 290

Qy     310 PQFDWLGYIKKVIDTRLYPHLKDISPSENVVVRVPQYFKDLFRILGSERKKTIANYLVWR 369
           | :||  ||             :   :  ||     |    :|       |:  :  ::
Db     291 PGYDWNRYIA----------ASGLPKVDRFVVTTNTTFPKYAKIYAETPLDTLKAWQAFK 340

Qy     370 MVYSRIPNLSRRFQYRWLEF-SRVIQGTTTLLPQWDKCVNFIESALPYVVGKMFVDVYFQ 428
           :  :  | ||:||     || :: : |     |:| : |  :   |   ||| :|  ||
Db     341 VTDNAAPLLSKRFVDAGFEFRNKTLAGQPEQRPRWKRGVGAVNGLLGEAVGKDYVAAYFP 400

Qy     429 EDKKEMMEELVEGVRWAF---IDMLEKENEWMDAGTKRKAKEKARAVLAKVGYPEFIMND 485
           : |  | |||  || |    || |    :|| | || ||:||      |:|||:
Db     401 PESKAKMLELVANVRGAMKVRIDNL----DWMSAETKVKAQEKLAKFTVKIGYPD----- 451

Qy     486 THVNEDLKAIKFSEADYFGNVLQTRKYLAQSDFFWLRKAVPKTEWFTNPTTVNAFYSAST 545
           | ||   ::  : | :|||  :   :    |   | | | ||||   | ||||:|::
Db     452 --VWEDYSKLEIKDNDAYGNVQRAGAWAFAKDVERLFKPVDKTEWGMTPQTVNAYYNSVN 509

Qy     546 NQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNGRKYDKNGNLDPWWST 605
           |:| |||  || |||     | :::|| || ::|||  ||||: ||| | :| |  ||:
Db     510 NEIVFPAAILQAPFFHPDADP-AINYGGIGGVIGHEIGHGFDDQGRKSDGDGVLRDWWTA 568

Qy     606 ESEEKFKEKTKCMINQYSNYYWKKAGLNVKGKRTLGENIADNGGLREAFRAYRKWINDRR 665
           |   ||| :   :  ||  :     |: : |  |:|||| | |||  |  |||  :
Db     569 EDAAKFKAQADRLGAQYGAFE-PLPGMKLNGALTMGENIGDMGGLAFALDAYRASL---- 623

Qy     666 QGLEEPLLPGITFTNNQLFFLSYAHVRCNSYRPEAAREQVQIGAHSPPQFRVNGAISNSE 725
           :|   |:| |  || :|  :| :| |     | || ::|:  | |||  :|||| | | |
Db     624 KGQPAPVLDG--FTGDQRVYLGWAQVWRGKQRDEALKQQIIAGPHSPGYYRVNGTIRNME 681

Qy     726 EFQKAFNCPPNSTM-----NRGMDSCRLW 749
           :  |::  |   :     ||     ::|
Db     682 GWYSAYDVKPGDKLYIAPENR----VKIW 706
```

Search completed: May 21, 2003, 18:50:01
Job time : 52 secs